

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:42:00 ; Search time 5070 Seconds

(without alignments)
10050.323 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800

Sequence: 1 acattcttcaaacctctta.....caataatcagcttgatg 800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31937310525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl: *
1: gb env: *
2: gb pal: *
3: gb ph: *
4: gb pl: *
5: gb pr: *
6: gb ro: *
7: gb sta: *
8: gb sy: *
9: gb un: *
10: gb vi: *
11: gb ov: *
12: gb hcg: *
13: gb in: *
14: gb om: *
15: gb pa: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798.4	99.8	120407	12 AP001967	AP001967 Homo sapi
2	798.4	99.8	165223	5 AC104059	AC104059 Homo sapi
3	796.8	99.6	175425	12 AC012208	AC012208 Homo sapi
4	397.8	49.7	401	7 G49140	G49140 SHGC-79840
5	233	29.1	206504	12 AC154950	AC154950 Bos tauru
6	113.2	14.2	181548	6 AC137121	AC137121 Mus muscu
7	110.8	13.8	206606	12 AC141145	AC141145 Rattus no
8	82.8	10.3	1422	2 BD249787	BD249787 Polypepti
9	82.8	10.3	1422	2 AR430630	AR430630 Sequence
10	82.8	10.3	1422	2 AX027295	AX027295 Sequence
11	82.8	10.3	1505	2 BD078044	BD078044 JNK3-cont
12	82.8	10.3	1505	2 CO892479	CO892479 Sequence
13	82.8	10.3	1505	2 AR380407	AR380407 Sequence
14	82.8	10.3	1505	2 AR716219	AR716219 Sequence
15	82.8	10.3	1505	2 AX377861	AX377861 Sequence
16	82.8	10.3	1505	5 HSU34819	U34819 Human JNK3
17	82.8	10.3	1850	5 BC065516	BC065516 Homo sapi
18	82.8	10.3	2095	5 AK091104	AK091104 Homo sapi

19	82.8	10.3	2211	2 CS206709	CS206709 Sequence
20	82.8	10.3	2366	2 BD078045	BD078045 JNK3-cont
21	82.8	10.3	2367	2 AR716220	AR716220 Sequence
22	82.8	10.3	2494	5 BC051731	BC051731 Homo sapi
23	82.8	10.3	2677	2 AR454561	AR454561 Sequence
24	82.8	10.3	2678	5 BC022492	BC022492 Homo sapi
25	82.8	10.3	2690	5 BC035057	BC035057 Homo sapi
26	82.8	10.3	2698	2 CS206710	CS206710 Sequence
27	82.8	10.3	3081	5 AK124791	AK124791 Homo sapi
28	80.4	10.1	1269	8 AY888567	AY888567 Synthetic
29	80.4	10.1	1269	8 AY890997	AY890997 Synthetic
30	80.4	10.1	1269	8 AY891216	AY891216 Synthetic
31	80.4	10.1	1269	8 AY893302	AY893302 Synthetic
32	80.4	10.1	1269	8 AY893752	AY893752 Synthetic
33	80.4	10.1	1269	8 BT019710	BT019710 Synthetic
34	80.4	10.1	1306	2 BD249786	BD249786 Polypepti
35	80.4	10.1	1306	2 AR430629	AR430629 Sequence
36	80.4	10.1	1306	2 AX027293	AX027293 Sequence
37	80.4	10.1	1773	2 BD078046	BD078046 JNK3-cont
38	80.4	10.1	1773	2 CO892477	CO892477 Sequence
39	80.4	10.1	1773	2 AR716221	AR716221 Sequence
40	80.4	10.1	1773	2 AX377859	AX377859 Sequence
41	80.4	10.1	2096	5 HSU34820	U34820 Human JNK3
42	80.4	10.1	2096	2 CO714411	CO714411 Sequence
43	80.4	10.1	2131	2 AR709626	AR709626 Sequence
44	80.4	10.1	2155	2 CS206711	CS206711 Sequence
45	80.4	10.1	2156	5 AK057723	AK057723 Homo sapi
46	80.4	10.1	2372	2 BD078047	BD078047 JNK3-cont
47	80.4	10.1	2372	2 BD078048	BD078048 JNK3-cont
48	80.4	10.1	2372	2 CS206708	CS206708 Sequence
49	80.4	10.1	2372	2 AR270826	AR270826 Sequence
50	80.4	10.1	2372	2 AR716222	AR716222 Sequence
51	80.4	10.1	2372	2 AR716223	AR716223 Sequence
52	80.4	10.1	2372	5 HSU07620	U07620 Human MAP k
53	80.4	10.1	2982	2 AR454560	AR454560 Sequence
54	80.4	10.1	8750	2 AX209898	AX209898 Sequence
55	68.4	8.6	1395	6 AB096077	AB096077 Mus muscu
56	68.4	8.6	1395	6 AB096079	AB096079 Mus muscu
57	68.4	8.6	2789	6 BC046625	BC046625 Mus muscu
58	66.8	8.3	1975	6 BD078049	BD078049 JNK3-cont
59	66.8	8.3	1975	2 CO892483	CO892483 Sequence
60	66.8	8.3	1975	2 AR716224	AR716224 Sequence
61	66.8	8.3	1975	2 AX377865	AX377865 Sequence
62	66.8	8.3	1975	6 RATSAP4C	RATSAP4C Sequence
63	66.8	8.3	1975	6 CO892481	CO892481 Sequence
64	66.8	8.2	1240	2 AX377863	AX377863 Sequence
65	66.8	8.2	1240	6 AB005665	AB005665 Mus muscu
66	66.8	8.2	1269	6 AB096076	AB096076 Mus muscu
67	66.8	8.2	1269	6 AB096078	AB096078 Mus muscu
68	64.4	8.1	2522	2 BD078050	BD078050 JNK3-cont
69	64.4	8.1	2522	2 AR716225	AR716225 Sequence
70	64.4	8.1	2522	6 MUSMAPK	L35236 Mus musculu
71	58.4	7.3	1522	13 AY701231	AY701231 Orconecte
72	58.4	7.2	176250	12 CR354555	CR354555 Datio rer
73	56.4	7.0	227676	6 AC154649	AC154649 Mus muscu
74	55.8	7.0	813	7 BV654723	BV654723 S216P201
75	55.8	7.0	48787	5 DQ066599	DQ066599 Homo sapi
76	55.8	7.0	80527	5 AC092290	AC092290 Homo sapi
77	55.8	7.0	115793	5 AC104115	AC104115 Homo sapi
78	54	6.8	2918	6 BC053027	BC053027 Mus muscu
79	53.2	6.7	254280	12 AC131372	AC131372 Rattus no
80	53.2	6.7	259608	12 AC131381	AC131381 Rattus no
81	52	6.5	106753	4 AC146706	AC146706 Medicago
82	52	6.5	119559	4 AC147484	AC147484 Medicago
83	52	6.5	127651	12 AC166237	AC166237 Medicago
84	51.8	6.5	161002	12 CR759944	CR759944 Datio rer
85	51.6	6.5	1197	6 AB005663	AB005663 Mus muscu
86	50.8	6.3	11008	6 RATSAPKD	L77123 Rattus norv
87	50.8	6.3	110000	12 PFMAL13_15	Continuatiion (16 o
88	50.6	6.3	177324	12 BX957228	BX957228 Datio rer
89	49.6	6.2	1877	11 BC109420	BC109420 Datio rer
90	49.6	6.2	11882	13 AC115612	AC115612 Dictyoste
91	49.4	6.2	580	2 AX526055	AX526055 Sequence

92 49.4 6.2 61052 12 AC123513 AC123513 Dictyoste
93 49.4 6.2 136240 13 AC117070 AC117070 Dictyoste
94 49.2 6.2 37983 5 D0027001 D0027001 Homo sapi
95 49.2 6.2 98146 5 AP002907 AP002907 Homo sapi
96 49.2 6.2 146570 13 AC117076 AC117076 Dictyoste
97 49.2 6.2 162130 12 AC021004 AC021004 Homo sapi
98 49.2 6.2 220215 5 AC009708 AC009708 Homo sapi
99 48.8 6.1 2372 2 AR719430 AR719430 Sequence
100 48.8 6.1 2372 2 AX748405 AX748405 Sequence

ALIGNMENTS

RESULT 1
LOCUS AP001967/c 120407 bp DNA linear HTG 06-JUN-2000
DEFINITION Homo sapiens chromosome 4 clone 2242B18 map 4q22-q24, ***
SEQUENCING IN PROGRESS ***, 3 unordered pieces.
ACCESSION AP001967
VERSION AP001967.1 GI:7678857
KEYWORDS HTG, HTGS, PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 120407)
Tsai,S.F.
Direct Submission
Submitted (28-APR-2000) Shih-Feng Tsai, National Yang-Ming
University, Institute of Genetics, 155 Li-Rong St. Section 2,
Peitou, Taipei, Taiwan 11221, Republic of China
(E-mail: ymdesai@ym.edu.tw, URL: http://genome.ym.edu.tw/
Tel:886-2-28267043, Fax:886-2-28264930)
Gaps between the contigs are represented as 100 N.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 87654: contig of 87654 bp in length
* 87655 87754: gap of 100 bp
* 87755 107685: contig of 19931 bp in length
* 107686 107785: gap of 100 bp
* 107786 120407: contig of 12622 bp in length.
Location/Qualifiers
1. 120407
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
/map="4q22-q24"
/clone="2242B18"

ORIGIN
Query Match 99.8%; Score 798.4; DB 12; Length 120407;
Best Local Similarity 99.8%; Pred. No. 1.5e-235;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATTTCTAAACCTTTATATAGTGTGAGCATAGGCTTAGGAAAAATATATAGCATT 60
DB 69536 ACAATTTCTAAACCTTTATATAGTGTGAGCATAGGCTTAGGAAAAATATATAGCATT 69467
QY 61 AATAAGTAATTTGTCTCAAGTCATACCTAAGACATTTAGTAGATCAGTAAAAATATAT 120
DB 69466 AATAAGTAATTTGTCTCAAGTCATACCTAAGACATTTAGTAGATCAGTAAAAATATAT 69407
QY 121 ATGCACATTTGTGTATTAATTTCTGTGGCTAGCAACGAAAAATTTCCAACTGACCTT 180

DB 69406 ATGCACATTTGTGTATTAATTTCTGTGGCTAGCAACGAAAAATTTCCAACTGACCTT 69347
QY 181 AACCGAGCCCATCTGGTAGATGTTTCAATATTTGTCACATCAACCTTGAGAGATTTC 240
DB 69346 AACCGAGCCCATCTGGTAGATGTTTCAATATTTGTCACATCAACCTTGAGAGATTTC 69287
QY 241 AAACACTAAGATGAATGAGGAAAGAGTAGCGGCTGAAAGGATTAAGTACCTCACTT 300
DB 69286 AAACACTAAGATGAATGAGGAAAGAGTAGCGGCTGAAAGGATTAAGTACCTCACTT 69227
QY 301 GACTTGTATGTCACAAAGGCACTTATGCTGATTTTGTAGAGGCACTTACCTCTTA 360
DB 69226 GACTTGTATGTCACAAAGGCACTTATGCTGATTTTGTAGAGGCACTTACCTCTTA 69167
QY 361 GCCCATGTTAATCTTTCTCAGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 69166 GCCCATGTTAATCTTTCTCAGATTCATTAATTAATTAATTAATTAATTAATTAATTAAT 69107
QY 421 TGTCCTGATCATTCACATCGAATATATCAGATGAATGCGACACTGATATCAAAAGAA 480
DB 69106 TGTCCTGATCATTCACATCGAATATATCAGATGAATGCGACACTGATATCAAAAGAA 69047
QY 481 AATAAATCTAATATATTAATTAAGACACACATGATTTTTCATCTGCTCTTTAG 540
DB 69046 AATAAATCTAATATATTAATTAAGACACACATGATTTTTCATCTGCTCTTTAG 68987
QY 541 CAATGTTATGTTATTTCTTTCGACCCCTACACAAAGGCCAAGAAATTAACAGATCTAG 600
DB 68986 CAATGTTATGTTATTTCTTTCGACCCCTACACAAAGGCCAAGAAATTAACAGATCTAG 68927
QY 601 TTTATGTTATTTACGAGAGATGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 68926 TTTATGTTATTTACGAGAGATGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68867
QY 661 ATTTTGTCTTTCTTCTCTGATTCATTAATTTCTGATTAATTTCTGATTAATTTCTGATTAAT 720
DB 68866 ATTTTGTCTTTCTTCTCTGATTCATTAATTTCTGATTAATTTCTGATTAATTTCTGATTAAT 68807
QY 721 CTGTGTTATTTAGAAAAACAATTTATCTTCATTCACAGGAAATTCATTAATTTATTC 780
DB 68806 CTGTGTTATTTAGAAAAACAATTTATCTTCATTCACAGGAAATTCATTAATTTATTC 68747
QY 781 CAATTAATTAATCTTTTATG 800
DB 68746 CAATTAATTAATCTTTTATG 68727

RESULT 2
LOCUS AC104059 165223 bp DNA linear PRI 21-FEB-2002
DEFINITION Homo sapiens BAC clone RP13-514E23 from 4, complete sequence.
ACCESSION AC104059
VERSION AC104059.5 GI:18677542
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 165223)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9847074
2 (bases 1 to 165223)
Wang, C. and Cotton, M.
The sequence of Homo sapiens BAC clone RP13-514E23
Unpublished (2001)
REFERENCE 3 (bases 1 to 165223)
Waterston,R.H.
Direct Submission
Submitted (03-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,

REFERENCES
 4 (bases 1 to 165223)
 AUTHORS
 TITLE
 JOURNAL
 MO 63108, USA
 5 (bases 1 to 165223)
 WATERSTON, R.
 DIRECT SUBMISSION
 Submitted (15-FEB-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 165223)
 WATERSTON, R.
 DIRECT SUBMISSION
 Submitted (21-FEB-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Feb 15, 2002 this sequence version replaced gi:18370036.

 Center: Genome Center

 Center: Washington University Genome Sequencing Center

 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@wustl.wustl.edu

 Summary Statistics

 Center project name: H_FH0514E23

 NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

 This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

 MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D.
 McPherson, Department of Genetics, Washington University, St. Louis
 MO. For additional information about the map position of this
 sequence, see http://genome.wustl.edu/gsc

 SOURCE INFORMATION:
 The RPCI-13 Human Female BAC library was constructed using improved
 cloning techniques developed by Kazutoyo Osoegawa. The library was
 generated by Baohui Zhao in our laboratory. Construction was
 funded by a grant from the National Human Genome Research Institute
 (NHGRI, NIH) (#1R01HG01165-03). The library was generated according
 to the new NHGRI/DOE 'Guidance on Human Subjects in Large-Scale DNA
 Sequencing'.
 Female blood was obtained via a double-blind selection protocol.
 Female blood DNA was isolated from one randomly chosen donor (out
 of 10 female donors) and partially digested with a combination of
 EcoRI and EcoRI Methylase for library segments 1k2 or either MboI
 or DpnII for library segments 3k4. Size selected DNA was cloned
 into the pBAC3.6 vector between the EcoRI sites for library
 segments 1k2 or the BamHI sites for library segments 3k4. The
 ligation products were transformed into DH10B electrocompetent
 cells (BRL Life Technologies). The library has been arrayed into
 384-well microtiter dishes and also gridded onto 22x22cm nylon high
 density filters for screening by probe hybridization.

 NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP13-375K17. Actual start of
 this clone is at base position 1 of RP13-514E23; actual end is at
 base position 165223 of RP13-514E23.
 Data from AC012208 was used to finish AC104059. Polymorphisms exist
 between AC012208 and AC104059.
 Location/Qualifiers
 1..165223
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

/chromosome="4"
 /map="4"
 /clone="RP13-514E23"
 /clone_1ib="RPCI-13"
 54..230
 /rpt_family="MIR"
 155..602
 /note="match to EST AI219433 (NID:g3801636) qh13a05.x1"
 repeat_region
 375..447
 /rpt_family="L2"
 repeat_region
 446..568
 /rpt_family="L2"
 repeat_region
 1528..1685
 /rpt_family="(TAGA)n"
 repeat_region
 1774..1819
 /rpt_family="(TAGG)n"
 repeat_region
 1916..2228
 /rpt_family="Alu"
 repeat_region
 2314..2725
 /rpt_family="L1"
 repeat_region
 2741..3010
 /rpt_family="L1"
 misc_feature
 2759..3201
 /note="match to EST BI020464 (NID:g14427094)"
 repeat_region
 3203..3345
 /rpt_family="L1"
 misc_feature
 4353..4368
 /note="match to EST AI689229 (NID:g4900523) cx82c06.x1"
 misc_feature
 4353..4368
 /note="match to EST BI963954 (NID:g16338359) i663b02.y1"
 misc_feature
 4353..4368
 /note="similar to Homo sapiens EST HI9314 (NID:g885554)
 ym44c03.s1"
 misc_feature
 4602..5135
 /note="match to EST AW264096 (NID:g6640912) xq83f12.x1"
 misc_feature
 4749..5495
 /note="match to EST AI761743 (NID:g5177499) wg67g07.x1"
 misc_feature
 4749..5416
 /note="similar to Mus musculus EST BI697031
 (NID:g15659660)"
 misc_feature
 4749..5269
 /note="match to EST AA993990 (NID:g3180535) ou42a04.s1"
 misc_feature
 4749..5200
 /note="similar to Homo sapiens EST BI520965
 (NID:g15345757)"
 misc_feature
 4749..5171
 /note="similar to Mus musculus EST AA879964 (NID:g2988947)
 vw02e03.x1"
 misc_feature
 4751..5458
 /note="match to EST BG181781 (NID:g13703468)"
 misc_feature
 4751..4876
 /note="match to EST BG186510 (NID:g13708197)"
 misc_feature
 4778..4859
 /note="match to EST BG204046 (NID:g13725733)"
 misc_feature
 4794..5096
 /note="match to EST AA216144 (NID:g1016083)"
 misc_feature
 4876..5060
 /note="match to EST BG204046 (NID:g13725733)"
 misc_feature
 4890..5494
 /note="similar to Mus musculus EST BM120254
 (NID:g17088280)"
 misc_feature
 4953..5470
 /note="similar to Mus musculus EST AA839645 (NID:g2915740)
 vw97g06.x1"
 misc_feature
 4955..5493
 /note="match to EST AW341386 (NID:g6838012) xz39e11.x1"
 misc_feature
 4985..5263
 /note="match to EST AI350609 (NID:g4087815) qg37e09.x1"
 misc_feature
 5041..5493
 /note="match to EST BG576372 (NID:g13584025)"
 misc_feature
 5079..5290
 /note="match to EST BG204046 (NID:g13725733)"
 misc_feature
 5163..5493

```

misc_feature      /note="match to EST A1767905 (NID:g5234414) w199a11.x1"
5292..5586
/note="similar to Mus musculus EST BB321301
(NID:g9029615)"
misc_feature      5368..5869
/note="match to EST AW401568 (NID:g6920254)"
repeat_region     5445..5472
/rpc_family="AT_rich"
misc_feature      6016..6179
/note="match to EST N28367 (NID:g1146603) yx26f08.r1"
misc_feature      6087..6807
/note="match to EST B1916286 (NID:g16180249)"
misc_feature      6183..6545
/note="similar to Homo sapiens EST AA132419 (NID:g1693910)
z007a10.r1"
misc_feature      6298
/note="match to EST BE737827 (NID:g10151819)"
misc_feature      6311..6864
/note="match to EST BE738433 (NID:g10152425)"
misc_feature      6314..6871
/note="match to EST BE737827 (NID:g10151819)"
repeat_region     6641..6790
/rpc_family="L2"
repeat_region     6830..6967
/rpc_family="MIR"
repeat_region     7012..7339
/rpc_family="Alu"
misc_feature      7175..7217
/note="match to EST BF854904 (NID:g12242648)"
repeat_region     7364..7390

```

Query Match 99.8%; Score 798.4; DB 5; Length 165223;

Best Local Similarity 99.8%; Pred. No. 1.5e-335; Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 ACATTTTCAAAACCTTTATAGTAGAGCATGTCTTAGAGAAAATATATAGCATT 60
DB 32840 ACATTTTCAAAACCTTTATAGTAGAGCATGTCTTAGAGAAAATATATAGCATT 32899
OY 61 AATAAGTAATTTGTCTCAAGTCATCTAAGCAATTAAGCATTAAGATCAGTAAATAAT 120
DB 32900 AATAAGTAATTTGTCTCAAGTCATCTAAGCAATTAAGCATTAAGATCAGTAAATAAT 32959
OY 121 ATGCACAAATTTGTCTCAAGTCATCTAAGCAATTAAGCATTAAGATCAGTAAATAAT 180
DB 32960 ATGCACAAATTTGTCTCAAGTCATCTAAGCAATTAAGCATTAAGATCAGTAAATAAT 33019
OY 181 AACCGAGGCCATCTGTAGATGTTTCAACTATTGTCACTCAACCTTGAGAGAGTTC 240
DB 33020 AACCGAGGCCATCTGTAGATGTTTCAACTATTGTCACTCAACCTTGAGAGAGTTC 33079
OY 241 AAACACTAAGATGAATGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 33080 AAACACTAAGATGAATGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 33139
OY 301 GACTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 33140 GACTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 33199
OY 361 GCCCATGTTAATTTCTTCAAGATTCATTAATTAATTAATTAATTAATTAATTAAT 420
DB 33200 GCCCATGTTAATTTCTTCAAGATTCATTAATTAATTAATTAATTAATTAATTAAT 33259
OY 421 TGCTCTGATCATTAACCATGAGATTAATGAGATGAGATGAGATGAGATGAGATGAG 480
DB 33260 TGCTCTGATCATTAACCATGAGATTAATGAGATGAGATGAGATGAGATGAGATGAG 33319
OY 481 ATAAATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
DB 33360 ATAAATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 33379
OY 541 CAATGTATATTTCTTCAACCCCTTCAACAAAGGCCAAGAAATTAACAAAGTACTAG 600

```

```

DB 33380 CAATGTATATTTCTTCAACCCCTTCAACAAAGGCCAAGAAATTAACAAAGTACTAG 33439
OY 601 TTTATTTGTTATTCACGAGAGTGAATCTGAGAGAGAGAGGCTGTCTTTTACTACACC 660
DB 33440 TTTATTTGTTATTCACGAGAGTGAATCTGAGAGAGAGAGGCTGTCTTTTACTACACC 33499
OY 661 ATTTTATGCTTTTCTTCTGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
DB 33500 ATTTTATGCTTTTCTTCTGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 33559
OY 721 CTGTGTTATTAAGAAACAAATTTATCTTCATCCACAGGAGAAATTAATTAATG 780
DB 33560 CTGTGTTATTAAGAAACAAATTTATCTTCATCCACAGGAGAAATTAATTAATG 33619
OY 781 CAATTAATTAATGTTTGAATG 800
DB 33620 CAATTAATTAATGTTTGAATG 33639

```

RESULT 3
AC012208/c 175425 bp DNA linear HTG 26-MAY-2000
LOCUS Homo sapiens chromosome 4 clone RP11-375K17 map 4, WORKING DRAFT
DEFINITION SEQUENCE, 12 unordered pieces.
AC012208
AC012208.3 GI:8096853
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS HTG; HTGS (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 175425)
Britten, B., Linton, L., Nussbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-375K17
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 175425)
Britten, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barne, N., Beckert, R., Bogdanovskiy, L., Bokhsalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collinmore, A., Cooke, P., Deatellano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., C. Johnson, R., Jones, C., Kam, L., Karatas, A., Klein, J., Lehoczek, J., Lieu, C., Locke, K., Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tittel, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On May 26, 2000 this sequence version replaced gi:6454052.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L1753
Center clone name: 375_K_17
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 144873 bases at least Q40
Consensus quality: 161974 bases at least Q30
Consensus quality: 170540 bases at least Q20

QY 721 CTGTGTTATATAGAAACAAATTATCTTCAATCCACAGGAAATTCATTACTTAATGC 780
 DB 136993 CTGTGTTATATAGAAACAAATTATCTTCAATCCACAGGAAATTCATTACTTAATGC 136934
 QY 781 CAATATATTACGTTTGATG 800
 DB 136933 CAATATATTACGTTTGATG 136914

RESULT 4
 G49140/c 401 bp DNA linear STS 30-MAR-2000
 LOCUS SHGC-79940 Human Homo sapiens STS genomic, sequence tagged site.
 DEFINITION G49140
 ACCESSION G49140.1 GI:4529800
 VERSION STS.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 401)
 OLIVER, M. and Cox, D. R.
 Unpublished, Oliver, M., Cox, D. R. (2000)
 JOURNAL Unpublished (2000)

REFERENCE
 AUTHORS Contact: Michael Oliver, David R. Cox
 TITLE Stanford Human Genome Center
 JOURNAL Stanford University School of Medicine
 4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
 Tel: (650) 320-5800
 Fax: (650) 320-5801
 Email: oliver@shgc.stanford.edu
 Primer A: TTGTGTAGGGGTGCAGAGAAT
 Primer B: CCACATGACTGATGTCACAAA
 STS size: 282

PCR Profile:
 Initial incubation: 95 degrees C for 10 minutes
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 60 degrees C for 30 seconds
 Polymerization: 72 degrees C for 23 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9700

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 AMPTag Gold Polymerase: 0.07 units/uM
 Total Vol: 5 uM

Buffer:
 MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3

FEATURES
 source BAC ends sequenced at TIGR from the RPC11 BAC library. Designed
 and developed at the Stanford Human Genome Center.
 Location/Qualifiers
 1..401
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="4"
 /clone_11b="Human"
 106..387
 106..128
 complement(365..387)

STS
 primer_bind
 primer_bind
 ORIGIN

Query Match 49.7%; Score 397.8; DB 7; Length 401;
 Best Local Similarity 99.5%; Pred. No. 1.9e-111;

Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 280 AGGATTACTAGCTCCACATTGATGATGTCGAAAGGCGATTATGCTGGAATTTG 339
 DB 401 AGGATTACTAGCTCCACATTGATGATGTCGAAAGGCGATTATGCTGGAATTTG 342
 QY 340 ATGAGGACATTTACCTTTAGCCCATGTGAATTTCTTACAGATTCATTATTA 399
 DB 341 ATGAGGACATTTACCTTTAGCCCATGTGAATTTCTTACAGATTCATTATTA 282
 QY 400 AATTATTTATGAAAAAGTTTGTCTGGATCATTCACATGATTAATCAGATGAATG 459
 DB 281 AATTATTTATGAAAAAGTTTGTCTGGATCATTCACATGATTAATCAGATGAATG 222
 QY 460 CCACACTGAATATCAAAAGAAATTAATAATCATTAATAGACACACACATGTGATA 519
 DB 221 CCACACTGAATATCAAAAGAAATTAATAATCATTAATAGACACACACATGTGATA 162
 QY 520 TTGTGCAATGCTCTTTTACGAATGTATATTTCTTGCACCCCTACCAAGGCC 579
 DB 161 TTGTGCAATGCTCTTTTACGAATGTATATTTCTTGCACCCCTACCAAGGCC 102
 QY 580 AAGAAATTACACAGTACTGTTTATGTTATTCACGAGAGTACTGAGAGAGA 639
 DB 101 AAGAAATTACACAGTACTGTTTATGTTATTCACGAGAGTACTGAGAGAGA 42
 QY 640 AGGCTGCTCTTTTACTACACCATTTTATGCTTTCTCTG 680
 DB 41 AGGCTGCTCTTTTACTACACCATTTTATGCTTTCTCTG 1

RESULT 5
 AC154950 206504 bp DNA linear HTG 01-JUL-2005
 LOCUS Bos taurus clone CH240-42G8, *** SEQUENCING IN PROGRESS ***, 29
 AC154950
 DEFINITION unordered pieces.
 AC154950
 VERSION AC154950.2 GI:68265244
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 206504)
 Muzny, D. Marie, Metker, M. Lee, Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
 Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
 Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guera, W.,
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
 Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
 Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
 Hollins, B., Howells, S., Huily, S., Hume, J., Idlebird, D., Jackson, A.,
 Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
 Karpachy, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowis, C., Kraft, C.L., Lebow, H., Levin, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
 Lorensuwa, L., Louisedge, H., Lozano, R. J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A.,
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mahoney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwankwelu, O., Okwuonu, G., Olarinmuse, A., Pal, S., Parks, K.,
 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
 Popper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L.,
 Puzio, M., Quito, J., Rachlin, E., Reeves, K., Regier, M., Reigh, R.,
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richard, S., Riggs, F.,
 Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.,
 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
 Shetty, D., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajda, D.,
 Sheehy, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J.,
 Steele, M., Strong, R., Sutton, A., Swack, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umanzi, K.,
 Valae, R., Vera, V., Villanueva, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Wilson, R., Wlezyk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhu, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 206504)
 Worley, K.C.
 Direct Submission
 Submitted (06-JAN-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 206504)
 Cow Genome Sequencing Consortium.
 Direct Submission
 Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jun 28, 2005 this sequence version replaced gi:57164422.
 The sequence in this assembly is a combination of BAC-based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: PCBU
 Center clone name: CH240-42G8
 ----- Summary Statistics
 Assembly program: Atlas 3.0?
 Consensus quality: 195434 bases at least Q40
 Consensus quality: 197609 bases at least Q30
 Consensus quality: 199501 bases at least Q20
 Estimated insert size: 200872; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 29 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.
 1 2091: contig of 2091 bp in length
 * 2092: gap of 871 bp
 * 2963: gap of 1741 bp in length
 * 4704: gap of 50 bp
 * 4753: contig of 1030 bp in length
 * 5784: gap of unknown length
 * 5884: contig of 673 bp in length
 * 6557: gap of 282 bp
 * 6838: gap of 4118 bp in length
 * 6839: contig of 3762 bp in length
 * 10956: gap of 50 bp
 * 11007: contig of 3762 bp in length
 * 14768: gap of 50 bp
 * 14818: contig of 2204 bp in length
 * 17023: gap of unknown length
 * 17123: contig of 7077 bp in length
 * 24200: gap of 50 bp
 * 24250: contig of 10444 bp in length
 * 34694: gap of 50 bp
 * 34744: contig of 6791 bp in length
 * 41534: gap of 50 bp
 * 41535: contig of 3804 bp in length
 * 41585: gap of 50 bp
 * 45388: contig of 4330 bp in length
 * 45438: gap of 50 bp
 * 45439: contig of 9640 bp in length
 * 49768: gap of 50 bp
 * 49818: contig of 2348 bp in length
 * 49819: gap of 50 bp
 * 59458: contig of 20100 bp in length
 * 59459: gap of 50 bp
 * 59508: contig of 2348 bp in length
 * 82756: gap of 50 bp
 * 82757: contig of 20100 bp in length
 * 82807: gap of 50 bp
 * 102907: contig of 13597 bp in length
 * 102957: gap of 50 bp
 * 118553: contig of 2564 bp in length
 * 118554: gap of 50 bp
 * 118604: contig of 263 bp in length
 * 121168: gap of 50 bp
 * 121431: contig of 9299 bp in length
 * 130730: gap of 50 bp
 * 130779: contig of 1477 bp in length
 * 130780: gap of 50 bp
 * 145257: contig of 2882 bp in length
 * 145307: gap of 50 bp
 * 145307: contig of 2882 bp in length
 * 173589: gap of 50 bp
 * 173638: contig of 12049 bp in length
 * 173639: gap of 50 bp
 * 185688: contig of 6894 bp in length
 * 185737: gap of 50 bp
 * 185738: contig of 50 bp
 * 192632: gap of 50 bp
 * 192681: contig of 4585 bp in length
 * 192682: gap of 50 bp
 * 197267: contig of 1007 bp in length
 * 197267: gap of 50 bp
 * 197366: contig of 1007 bp in length
 * 197366: gap of 50 bp
 * 198374: contig of 1564 bp in length
 * 198374: gap of 50 bp
 * 198474: contig of 1455 bp in length
 * 200038: gap of 50 bp
 * 200038: contig of 1455 bp in length
 * 200138: gap of 50 bp
 * 201592: contig of 1493 bp in length
 * 201593: gap of 50 bp
 * 201692: contig of 1493 bp in length
 * 203185: gap of 50 bp
 * 203285: contig of 1043 bp in length
 * 203286: gap of 50 bp
 * 204328: contig of 1043 bp in length
 * 204329: gap of 50 bp
 * 204428: contig of 2076 bp in length
 * 204429: gap of 50 bp
 * 206504: contig of 2076 bp in length.

FEATURES
 source
 1. 206504
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9913"
 /clone="CH240-42G8"
 2092. 2962
 /estimated_length=871
 4704. 4753
 /estimated_length=50
 5784. 5883
 /estimated_length=unknown
 6557. 6838
 /estimated_length=282
 10957. 11006

Query Match 29.1%; Score 233; DB 12; Length 206504;
 Best Local Similarity 68.6%; Pred. No. 8.8e-61;
 Matches 477; Conservative 0; Mismatches 185; Indels 33; Gaps 10;

	AC137121	181548 bp	DNA	linear	ROD 16-OCT-2004
LOCUS	AC137121				
DEFINITION	Mus musculus chromosome 5, clone RP23-286M22, complete sequence.				
ACCESSION	AC137121				

Query 115 ATATATATGCAATGTGTATTGATTCCTGCTAGCAACG--AAAAATTTCCAG 172
 11419 ATGTATATGTAAGTATGTGCTATTTTGTAGCTGCAAAATGTAAGATTTTCTGTG 11478
 173 CTGACCTTAACCGGACCCCACTGTGTAAGTGTTCACATTTGTCACATCAACCTGAG 232
 11479 CTGACTTATATGAGCCCGCTGTGTGTTAAGGCTTAACACTGTCACATCAACCTTAA 11538
 233 AAGAGTTCAACCACTAAGATGATGAGGAGAGAGT---AGCGGCTGAAAGATTAAT 288
 11539 AAGAGT---AAGCTTAAAGTGAATGAAGGAAAGGTTTAAAGTGAGGAGATTTCTCT 11595
 289 GAGCTTCAATGATCTGATGTCAAAAGGCGCTTATGCTGCAATTTTGTATGAGGCAC 348
 11596 GAACTTCAACACGAGGTGGTGTGCAAGAGGCACTTATGATCTGAATTTTGAAGAGAC 11655
 349 ATTACCTTTTGGCCATGTTACATTTTCTCAGAGTTCATTAATTAATTAATTTTA 408
 11656 ACCACCCCTTTA-----ATCAGATTAATGCTTAATTTTCTTAAGATT---CTTGTGTA 11705
 409 TGAAGAAAGTTTGTCTGATCATTAACATCAGAAATTAATCAGAAATGAAATGCCACACT 468
 11706 TTTTAAAGTTTGAAGAACTGATGTAATCATTTATGTCAGAAATTAATTAATGACACTTA 11765
 469 AATTCAAA---GAATTAATTAATTAATTTTAAAGACACACACATGTAATTTGTC 525
 11766 CCAATTCAAAAGGCGAGAGACATGAAATCATTAAGAGGAAAGAGGTA-ATCTAAGCTGT 11824
 526 CATGCTCTTTAAGCAATGTTATGTTTCTTGCAACCCCTACCAAGGCGCAGAA 585
 11825 CATATGCTTGATAGCA-----GTATTAATTTGATGCAATCTTCTTTAAGGCCAAGAAA 11879
 586 TTACACAAAGTACTAGTTATTTGTTATTCACGAGAGTGAAGTACTGAAGAGAGAGCTG 645
 11880 ATACGCAAGTACCGGTTTGTGTATTAATCAATGAGTGAAGTGAAGGAGAGAGCTG 11939
 646 TCCCTTTTACTACCACTTTTATGCTTTTCTTGTGATTCATTAATTTCTTGTAGATTA 705
 11940 TCCCTTTTACAAAGCCCAATCTTCTTCTTCTTCTTCCGAGTTCAATTAATTTTAAAGTAA 11999
 706 TTCTGTAAAGAAAGAGCTGTTTATTAAGAAACAAATTAATCTTCATCAACAGAGGAAA 765
 12000 TTCTGTAAAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 12058
 766 TTCTACTTAAATGCAAAATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 800
 12059 GTCA-----TTTATTAACAAACAAATTAATTAATTTGATG 12089

VERSION AC137121.9 GI:54261924
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

2 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

3 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

4 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

5 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

6 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

7 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

8 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

9 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

10 (bases 1 to 181548)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baerlein, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fairo, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retra, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., and Zody, M.

TITLE
JOURNAL

COMMENT

Phunhkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
 Recta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,
 Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J.,
 Topham, K., Travers, M., Vassiliev, H., Venkatakrishnan, V. S., Viel, R.,
 Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
 Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (16-OCT-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Oct 16, 2004 this sequence version replaced gi:51315566.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@road.mit.edu
 Project Information
 Center project name: L26408
 Center clone name: 286_M_22

FEATURES

source
 Location/Qualifiers
 1. 181548
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="5"
 /map="5"
 /clone="RP23-286M22"
 /clone_lib="RPCI-23 Female Mouse BAC"
 602. 647
 /rpt_family="(TG)n"
 repeat_region
 648. 827
 /rpt_family="(TG)n"
 complement(1596..1764)
 repeat_region
 2191..2303
 /rpt_family="Tigster7"
 repeat_region
 4661..4921
 /rpt_family="(TCTCCC)n"
 repeat_region
 5655..5755
 /rpt_family="L1MB8"
 repeat_region
 5793..5863
 /rpt_family="(TG)n"
 repeat_region
 5888..6000
 /rpt_family="(TG)n"
 repeat_region
 6014..6091
 /rpt_family="(TG)n"
 repeat_region
 6153..6269
 /rpt_family="(TG)n"
 repeat_region
 6288..6311
 /rpt_family="AT_rich"
 repeat_region
 complement(6312..6758)
 repeat_region
 /rpt_family="Lx2B"
 complement(6813..6853)
 repeat_region
 /rpt_family="B3A"
 6854..6875
 /rpt_family="(TA)n"
 repeat_region
 complement(6876..7024)
 repeat_region
 /rpt_family="B3A"
 7133..7181
 /rpt_family="(GA)n"
 repeat_region
 7775..7842
 /rpt_family="(GA)n"
 repeat_region
 8626..8662
 /rpt_family="(CAA)n"
 repeat_region
 complement(11814..12121)
 repeat_region
 /rpt_family="Lx"
 12627..12694
 /rpt_family="(GCAA)n"
 repeat_region
 13907..13933

/rpt_family="(CA)n"
 14706..14843
 /rpt_family="RMRER15"
 complement(15326..17003)
 repeat_region
 /rpt_family="L1VL2"
 18283..18311
 /rpt_family="AT_rich"
 20110..20146
 /rpt_family="(T)n"
 repeat_region
 20158..20182
 /rpt_family="(T)n"
 complement(20183..20327)
 repeat_region
 /rpt_family="B1_MM"
 20465..20649
 /rpt_family="L1MA6"
 20748..20905
 /rpt_family="L1MA6"
 20949..21648
 /rpt_family="L1MA6"
 21751..21847
 /rpt_family="B1_MM"
 21853..21904
 /rpt_family="(CAAAA)n"
 23773..23796
 /rpt_family="AT_rich"
 complement(24150..24474)
 repeat_region
 /rpt_family="ORR1A2"
 complement(24769..24950)
 repeat_region
 /rpt_family="B3A"
 25195..25696
 /rpt_family="R1TR11A"
 25813..25856
 /rpt_family="(CAGA)n"
 25884..25990
 /rpt_family="(GA)n"
 repeat_region
 complement(26526..27115)
 repeat_region
 /rpt_family="L1_MM"
 27187..27472
 /rpt_family="MTE"
 complement(28452..28558)
 repeat_region
 /rpt_family="L2"
 complement(29177..29528)
 repeat_region
 /rpt_family="MT2A"
 29537..29558
 /rpt_family="AT_rich"
 29760..29936
 /rpt_family="B2_Mm2"
 29945..29982
 /rpt_family="(TAAA)n"
 30905..30939
 /rpt_family="(A)n"

Query Match 14.2%; Score 113.2; DB 6; Length 181548;
 Best Local Similarity 65.0%; Pred. No. 9,7e-24;
 Matches 238; Conservative 0; Mismatches 108; Indels 20; Gaps 4;

QY 438 ATCAAGATATATAGATGATATGATCCACACTGGAATATCAAAAGAAATTAATCAAT 497
 DB 88752 ACCAGAAATTTAGACGATTTGATGATGATGATTAATAATAATAAACAACATCGAAAT 88811
 QY 498 ATTAAGACACACACATGTGATTTTGTCCATCTGCTCTTTAAGCAATGTTATTTTC 557
 DB 88812 ACGAGGAAACGCCCATGTGATATCTGTTCGCCAGGCTCTGTGACGGCATTC-----TC 88864
 QY 558 TTGCAACCCCTTACACAAAGGCCAAGAAATTAACAAGTACTGATTATTTGTTATTCACG 617
 DB 88865 TATGACCAACACCCGTCACAGGGCTGA-----AGACACGAGCTTCTGTGTTATTCACG 88917
 QY 618 GAGAGTGATACCTTAAGAGAGAGGCTGCTTTTACTACACATTTTATAGCTTTCTT 677
 DB 88918 GAGAGTGATACCTTAAGAGAGGCTGCTTTTACTACACATTTTATAGCTTTCTT 88977
 QY 678 CTGAATTCATTACTTCTTTAGATTAAGTTCTGTA-----AGAAACAGCTGTGTTATTATA 733

Db	88978	CTGAGTTCATACCTCCCTGTGGAGTAAGTTCTGTAAATCAACAATAATCGCCTCGTTATTATTA	8903
Oy	734	--GAACAATTTATCTTATCTTATCTCACAGGGAATTCATTACTTAATGCCAATTAATTC	791
Db	89038	ACAAAAGGAGAAGATTCCTTATTAATCAAAACCCTGCAGTCGCTAAATGMAAAAAATCACTT	89097
Oy	792	GTTTGG	797
Db	89098	TTCGCTG	89103
RESULT 7.			
LOCUS	AC141145		
DEFINITION	Rattus norvegicus clone CH230-140B2. WORKING DRAFT SEQUENCE, 51		
ACCESSION	AC141145	206606 bp	DNA linear HTG 05-APR-2003
VERSION	AC141145.3	GI:29568005	
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 206606)		
AUTHORS	Muzny,D.,Maize,M.,Metzker,M.,Lee,S.,Abramson,S.,Adams,C.,Alder,J.,Allen,C.,Allen,H.,Alsbrooks,S.,Amin,A.,Angularo,D.,Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,Balwin,D.,Bandaranaike,D.,Bader,M.,Barstead,M.,Benhammed,F.,Blawalo,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,Bryan,N.,Buhaq,C.,Burck,P.,Burrell,K.,Calderon,E.,Cardenas,V.,Carter,K.,Cavaero,I.,Ceasar,H.,Center,A.,Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,Devila,M.L.,Davis,C.,Day-Carroll,L.,De Anda,C.,Dederich,D.,Delgado,O.,Denison,S.,Deramo,C.,Ding,Y.,Dinh,H.,Divya,K.,Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Duval,B.,Eaves,K.,Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,Fernandes,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,M.,Foster,P.,Fraser,C.M.,Gabris,A.,Gante,R.,Garcia,A.,Garra,T.,Gaza,M.,Gebregorgis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,W.,Guevara,W.,Gunaratne,P.,Haaland,M.,Hamil,C.,Hamilton,C.,Hamilton,K.,Harvey,Y.,Haylak,P.,Hawes,A.,Henderson,N.,Hernandez,J.,Hernandez,R.,Hines,S.,Hladun,S.L.,Hodgeson,A.,Hogues,M.,Hollins,B.,Howells,S.,Huily,S.,Hume,J.,Idelbit,D.,Jackson,A.,Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolyet,A.,Karpatchy,S.,Kelly,S.,Kelly,S.,Khan,Z.,King,L.,Kovay,C.,Kowis,C.,Kraft,C.L.,Lebow,H.,Leyvan,J.,Lewis,L.,Li,Z.,Liu,J.,Liu,J.,Liu W., Liu Y., London,P.,Longacre,S., Lopez,J., Lorentzenwa,L.,Louisged,H.,Lozado,R.J.,Lu,X.,Ma,D.,Maheshwari,M.,Mahindartine,M.,Mahnoud,M.,Mailloy,K.,Manungu,A.,Manungu,B.,Mapua,P.,Martin,K.,Martin,R.,Martinez,E.,Mawhinney,S.,McLeod,M.,McNeill,T.,Meenen,E.,Milosavljevic,A.,Miner,G.,Mnjia,E.,Montemayor,J.,Moore,S.,Monkman,M.,Morris,K.,Morris,S.,Mundasa,M.,Murphy,M.,Natr,L.,Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,Okochelemeh,O.,Okumu,G.,Olarinuagason,A.,Pal,S.,Parks,K.,Pasernak,S.,Paul,H.,Perez,A.,Perez,L.,Plankkoch,C.,Plopper,F.,Poindexter,A.,Popovic,D.,Primus,E.,Pu,L.-L.,Piazto,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reigh,R.,Reilly,B.,Reilly,M.,Ren,Y.,Rauter,M.,Richards,S.,Riggs,F.,Rives,C.,Rodkey,T.,Rojaas,A.,Rose,M.,Rose,R.,Ruiz,S.J.,Sanders,W.,Savery,G.,Schetter,S.,Scott,G.,Shatman,S.,Shen,H.,Shetty,J.,Shvartsbeyn,A.,Slisom,I.,Sitter,C.D.,Smajs,D.,Sheed,A.,Sodergren,S.,Song,X.-Z.,Sotelle,R.,Sosa,J.,Steinle,M.,Strong,R.,Sutton,A.,Swatek,A.,Tabori,P.,Taylor,C.,Taylor,T.,Thomas,N.,Thomas,S.,Trejcek,A.,Trejos,Z.,Usumani,K.,Valas,R.,Vera,V.,Villasana,D.,Waldron,L.,Walker,B.,Wang,J.,Wang,Q.,Wang,S.,Warren,J.,Watson,R.,Wei,X.,White,F.,Williams,G.,Wilson,R.,Wlaczky,R.,Wooden,H.,Worley,K.,Wright,D.,Wright,R.,Mu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,Yu,F.,Zhang,J.,Zhou,J.,Zhou,X.,Zhao,S.,Zhu,D., von Niederhausen,A.,Weiser,K.,Smith,D.R.,		

TITLE	Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 206606)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (10-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 206606)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (05-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Apr 5, 2003 this sequence version replaced gi:28913313.
	----- Genome Center -----
	Center: Baylor College of Medicine
	Center code: BCM
	Web site: http://www.hgsc.bcm.tmc.edu/
	Contact: hgsc-help@bcm.tmc.edu
	----- Project Information -----
	Center project name: KEC
	Center clone name: CH230-140B2
	----- Summary Statistics -----
	Sequencing vector: Plasmid;
	Chemistry: Dye-terminator Big Dye; 100% of reads
	Assembly program: Phrap; version 0.990329
	Consensus quality: 191161 bases at least Q40
	Consensus quality: 195784 bases at least Q30
	Consensus quality: 199697 bases at least Q20
	Estimated insert size: 195646; sum-of-coverage
	Quality coverage: 3x in Q20 bases; sum-of-coverage

	* NOTE: Estimated insert size may differ from sequence length
	* (see http://www.hgsc.bcm.tmc.edu/docs/genbankdraft_data.html)
	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 51 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.

	* 1 1358: contig of 1358 bp in length
	* 1359 1458: gap of unknown length
	* 1459 2825: contig of 1367 bp in length
	* 2826 2925: gap of unknown length
	* 2926 4338: contig of 1413 bp in length
	* 4339 4438: gap of unknown length
	* 4439 5980: contig of 1542 bp in length
	* 5981 6080: gap of unknown length
	* 6081 7681: contig of 1601 bp in length
	* 7682 7781: gap of unknown length
	* 7782 9244: contig of 1463 bp in length
	* 9245 9345: gap of unknown length
	* 9345 10471: contig of 1127 bp in length
	* 10472 10571: gap of unknown length
	* 10572 11748: contig of 1177 bp in length
	* 11749 11848: gap of unknown length
	* 11849 13253: contig of 1405 bp in length
	* 13254 13353: gap of unknown length
	* 13354 14587: contig of 1234 bp in length
	* 14588 14687: gap of unknown length
	* 14688 16037: gap of unknown length
	* 16038 16137: gap of unknown length
	* 16138 17435: contig of 1298 bp in length
	* 17436 17535: gap of unknown length
	* 17536 18972: contig of 1437 bp in length
	* 18973 19072: gap of unknown length
	* 19073 21193: contig of 2121 bp in length
	* 21194 21293: gap of unknown length
	* 21294 23612: contig of 2319 bp in length

```

* 23613 23712: gap of unknown length
* 23713 26628: contig of 2916 bp in length
* 26629 26728: gap of unknown length
* 26729 29705: contig of 2978 bp in length
* 29707 29806: gap of unknown length
* 29807 32797: contig of 2991 bp in length
* 32798 32897: gap of unknown length
* 32898 35764: contig of 2867 bp in length
* 35765 35865: gap of unknown length
* 35866 38592: contig of 2728 bp in length
* 38593 38692: gap of unknown length
* 38693 42144: contig of 3452 bp in length
* 42145 42244: gap of unknown length
* 42245 43735: contig of 1490 bp in length
* 43735 43835: gap of unknown length
* 43835 46614: contig of 2780 bp in length
* 46615 46714: gap of unknown length
* 46715 48690: contig of 1976 bp in length
* 48691 48790: gap of unknown length
* 48791 51799: contig of 3009 bp in length
* 51800 51899: gap of unknown length
* 51900 54374: contig of 2475 bp in length
* 54375 54474: gap of unknown length
* 54475 58651: contig of 4177 bp in length
* 58652 58751: gap of unknown length
* 58752 61050: contig of 2299 bp in length
* 61051 61150: gap of unknown length
* 61151 64066: contig of 2916 bp in length
* 64067 64166: gap of unknown length
* 64167 67348: contig of 3182 bp in length
* 67349 67448: gap of unknown length
* 67449 70246: contig of 2798 bp in length
* 70247 70346: gap of unknown length
* 70347 73068: contig of 2722 bp in length
* 73069 73168: gap of unknown length
* 73169 76539: contig of 3371 bp in length
* 76540 76639: gap of unknown length
* 76640 81735: contig of 5096 bp in length
* 81736 81835: gap of unknown length
* 81836 85133: contig of 3298 bp in length
* 85134 85233: gap of unknown length
* 90585: contig of 5352 bp in length
* 90586 90685: gap of unknown length
* 90686 95785: contig of 5100 bp in length
* 95786 95885: gap of unknown length
* 95886 99327: contig of 3442 bp in length
* 99328 99427: gap of unknown length
* 99428 104621: contig of 5194 bp in length
* 104622 104721: gap of unknown length
* 104722 111646: contig of 6925 bp in length
* 111647 111746: gap of unknown length
* 111747 115420: contig of 3674 bp in length
* 115421 115520: gap of unknown length
* 115521 120264: contig of 4744 bp in length
* 120265 120364: gap of unknown length
* 120365 125661: contig of 5297 bp in length
* 125662 125761: gap of unknown length
* 125762 134249: contig of 8488 bp in length
* 134250 134349: gap of unknown length
* 134350 140554: contig of 6105 bp in length
* 140555 140554: gap of unknown length
* 140555 147949: contig of 7395 bp in length
* 147950 148049: gap of unknown length
* 148050 156077: contig of 8028 bp in length
* 156078 156177: gap of unknown length
* 156178 166426: contig of 10249 bp in length
* 166427 166526: gap of unknown length
* 166527 176298: contig of 9772 bp in length

```

```

Query Match 13.8%; Score 110.8; DB 12; Length 206606;
Best Local Similarity 80.2%; Pred. No. 5.3e-23;
Matches 130; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```

```

QY 581 AGAATTAACACAGTACTAGTTATTGGTTATTCACGGAGAGTACCTGAAGAGAA 640
DB 102768 AGGAAAGACACAGACTGCTCTTGTTATTCACGGAGAGTACCTGAAGAGAG 102827
QY 641 GGCTGCTCTTTACTACACCATTTTATGCTTTCTTGAATTCATTACTCTGTAG 700
DB 102828 GGCTGCTCTTTACTACACCATTTTATGCTTTCTTGAATTCATTACTCTGTAG 102887
QY 701 ATAGTCTCTTGAAGAAACAGCTGTATTATTAAGAAAACAA 742
DB 102888 ATAGTCTCTTGAAGAAACAGCTGTATTATTAAGAAAACAA 102929

```

```

RESULT 8
LOCUS BD249787/c 1422 bp DNA linear PAT 17-JUL-2003
DEFINITION Poly peptides derived from JNK3.
ACCESSION BD249787
VERSION BD249787.1 GI:33059557
KEYWORDS JP 2002534982-A/23.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

```

```

REFERENCE 1 (bases 1 to 1422)
AUTHORS Desanlis,F., Fournier,A., Maury,I. and Liu,Q.Z.
TITLE Poly peptides derived from JNK3
JOURNAL Patent: JP 2002534982-A 23 22-OCT-2002;
AVENTIS PHARMA SA

```

```

COMMENT OS Homo sapiens (human)
PN JP 2002534982-A/23
PD 22-OCT-2002
PF 19-JAN-2000 JP 2000594932
PR 20-JAN-1999 FR 99/00586; 26-FEB-1999 US 60/122175 PI
FRANCINE DESANLIS, ALAIN FOURNIER, ISABELLE MAURY, QING ZHOU LIU PC
C12N15/09, A61K39/395, A61K45/00, A61P7/10, A61P9/00, A61P25/00, PC
A61P25/14,
PC A61P25/16, A61P25/28, C07K16/40, C12N1/15, C12N1/19, C12N1/21 PC
, C12N5/10, C12N9/12,
PC C12Q1/02, C12Q1/48, C12N15/00, C12N5/00
CC Poly peptides derived from JNK3
FH Key location/Qualifiers
FT CDS (142)..(1419).

```

```

FEATURES
source location/Qualifiers
1..1422
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="caxon:9606"

```

ORIGIN

```

Query Match 10.3%; Score 82.8; DB 2; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GAACTGAAGAGAGAGGCTGCTTTTACTACACATTTTATGCTTTCTTGAATTC 685
DB 1283 GAACTGAAGAGAGAGGCTGCTTTTACTACACATTTTATGCTTTCTTGAATTC 1224
QY 686 ATTACTCTCTTGAATTAAGTTCTGT 711
DB 1223 ATTACTCTCTTGAATTAAGTTCTTT 1198

```

```

RESULT 9
LOCUS AR430630/c 1422 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 24 from patent US 6649388.
ACCESSION AR430630
VERSION AR430630.1 GI:40191471
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

```


Unclassified.
1 (bases 1 to 1422)
REFERENCE
Fournier,A., Maury,I., Zhou-Liu,Q. and Desanlis-Cremond,F.
TITLE
Polypeptides derived from JNK3
Patent: US 6649388-A 24 18-NOV-2003;
JOURNAL
Aventis Pharma S.A.; Antony;
FRX;
FEATURES
source
1. .1422
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGGAATTC 685
1283 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGGAATTC 1224
DB 686 ATTACTCTCTGTAGATAGTTCTGT 711
1223 ATTACTCTCTGTAGATAGTTCTTT 1198
QY 1223
RESULT 10
AX027295/c 1422 bp DNA linear PAT 16-SEP-2000
LOCUS
Sequence 24 from Patent WO04354.
DEFINITION
AX027295
ACCESSION
VERSION
AX027295.1 GI:10188271
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
Desanlis,F., Zhou-Liu,Q., Fournier,A. and Maury,I.
AUTHORS
Polypeptides derived from Jnk3
Patent: WO 0043524-A 24 27-JUL-2000;
JOURNAL
AVENTIS PHARMA SA (FR) ; DESANLIS FRANCINE (FR) ; ZHOU LIU QING
(FR) ; FOURNIER ALAIN (FR) ; MAURY ISABELLE (FR)
FEATURES
source
1. .1422
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
142. .1422
/note="unassigned protein product"
/codon_start=1
/protein_id="CAC09126.1"
/db_xref="GI:10188272"
/translation="MSKSKVNDQFVSEVSDSTFTVLKRYONLKPISGAOGIVCAAY
DYLDRNVAILKLSRPNQTHAKRAYRELVLKMCNHNKILSLVFPPOKTLSEGO
DYLVNMLDANICQYIOMELDERMSYLLIOMLGGIKLHSGITHRDLKRPENITVK
SDCTLIKILFGLARTAGTSFMTYVAVTRRAEVLILGMYENVDIVSVCIMGEM
VRKILIFPGRIYIDQNNKYIEQLGPCPEFMKLOPTVNVYENRPRKAGLTFPKLFP
DSLFPADSEHNKLSKASQARDLSKMLVIDPAKLSVDDALQHYIIVWYDPAVEAP
POLYDOLDERETIEEMKELIYKEVNVSEKTKNGVVKQPEPQGAANVSSESLPDS
SSVNDISSNSTDOTLASDIDSLSAASAPLGCGR"
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGGAATTC 685
DB 1283 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGGAATTC 1224
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
1223 ATTACTCTCTGTAGATAGTTCTTT 1198

DB 1223 ATTACTCTCTGTAGATAGTTCTTT 1198
RESULT 11
BD078044/c 1505 bp DNA linear PAT 27-AUG-2002
LOCUS
JNK3-controller and method of using the same.
DEFINITION
BD078044
ACCESSION
BD078044.1 GI:22623647
VERSION
JP 2001519146-A/1.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified sequences.
1 (bases 1 to 1505)
REFERENCE
1
Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.Y. and
Yang,D.D.
TITLE
JNK3-controller and method of using the same
JOURNAL
Patent: JP 2001519146-A 1 23-OCT-2001;
UNIVERSITY OF MASSACHUSETTS
COMMENT
OS Unidentified
PN JP 2001519146-A/1
PD 23-OCT-2001
PE 05-OCT-1998 JP 2000514991
PR 03-OCT-1997 US 60/060995
PI ROGER J DAVIS,RICHARD A FLAVELL,PASKO RAKIC,ALAN J WHITMARSH
PI ,CHIA YIN KUAN,
PI DERK DI YANG
PC C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
PC A61P21/00,
PC A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C12Q1/48,PC
C12Q1/68,
PC G01N33/15,G01N33/50,C12N15/00,C12N5/00
CC Strandedness: Double;
CC Topology: Linear;
CC JNK3-controller and method of using the same
FT Key
FT source 1. .1505
/organism="Unidentified".
FEATURES
source
1. .1505
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity 97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGGAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGGAATTC 1264
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
1263 ATTACTCTCTGTAGATAGTTCTTT 1238
RESULT 12
CO892479/c 1505 bp DNA linear PAT 01-NOV-2004
LOCUS
Sequence 56 from Patent EP1469316.
DEFINITION
CO892479
ACCESSION
CO892479.1 GI:55165021
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
Wehne,E.D., Schaefer,M.K., Gillen,C., Wetzel,S. and Wendt,S.

TITLE Screening method
JOURNAL Patent: EP 1469316-A 56 20-OCT-2004;
FEATURES Gruenenthal GmbH (DE)
SOURCE Location/Qualifiers
1. .1505
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity 97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 685
DB 1323 GCACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 1264

QY 686 ATTACTTCTTGTAGATAAGTTCTGT 711
DB 1263 ATTACTTCTTGTAGATAAGTTCTTT 1238

RESULT 13
AR380407/c. 1505 bp DNA linear PAT 18-DEC-2003
LOCUS AR380407
DEFINITION Sequence 952 from patent US 6607879.
ACCESSION AR380407
VERSION AR380407.1 GI:40088041
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1505)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 952 19-AUG-2003;
FEATURES Incyte Corporation; Palo Alto, CA
source Location/Qualifiers
1. .1505
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity 97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 685
DB 1323 GCACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 1264

QY 686 ATTACTTCTTGTAGATAAGTTCTGT 711
DB 1263 ATTACTTCTTGTAGATAAGTTCTTT 1238

RESULT 14
AR716219/c. 1505 bp DNA linear PAT 07-OCT-2005
LOCUS AR716219
DEFINITION Sequence 1 from patent US 6943000.
ACCESSION AR716219
VERSION AR716219.1 GI:77364280
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1505)
AUTHORS Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.-Y. and Yang,D.D.
TITLE JNK3 modulators and methods of use
JOURNAL Patent: US 6943000-A 1 13-SEP-2005;

University of Massachusetts and Yale University; Boston, MA
FEATURES Location/Qualifiers
1. .1505
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity 97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 685
DB 1323 GCACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 1264

QY 686 ATTACTTCTTGTAGATAAGTTCTGT 711
DB 1263 ATTACTTCTTGTAGATAAGTTCTTT 1238

RESULT 15
AX377861/c. 1505 bp DNA linear PAT 18-MAR-2002
LOCUS AX377861
DEFINITION Sequence 56 from Patent WO0212338.
ACCESSION AX377861
VERSION AX377861.1 GI:19573951
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gillen,C., Wetzel,J., Whendt,S., Weihe,E. and Schaefer,M.K.
TITLE Screening method
JOURNAL Patent: WO 0212338-A 56 14-FEB-2002;
FEATURES Gruenenthal GmbH (DE)
source Location/Qualifiers
1. .1505
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 1505;
Best Local Similarity 97.7%; Pred. No. 3.9e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 685
DB 1323 GCACCTGAAGAGAGAGGCTGCTCTTTTACACACCATTTTACGTTCTTCTGGAATTC 1264

QY 686 ATTACTTCTTGTAGATAAGTTCTGT 711
DB 1263 ATTACTTCTTGTAGATAAGTTCTTT 1238

RESULT 16
HSU34819 1505 bp mRNA linear PRI 25-JUL-1996
LOCUS HSU34819
DEFINITION Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.
ACCESSION U34819
VERSION U34819.1 GI:1463124
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1505)
AUTHORS Gupta,S., Barrett,T., Whitmarsh,A.J., Cavanagh,J., Sluss,H.K., Derjard,B. and Davis,R.J.
TITLE Selective interaction of JNK protein kinase isoforms with

JOURNAL EMBO J. 15 (11), 2760-2770 (1996)
 PUBMED 8654373
 REFERENCE 2 (bases 1 to 1505)
 AUTHORS Davis, R.J.
 TITLE Direct Submission
 JOURNAL Submitted (25-AUG-1995) Roger J. Davis, Molecular Medicine, University of Massachusetts Medical School, 373 Plantation Street, Worcester, MA 01605, USA

FEATURES
 source
 1. 1505
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="brain"
 1. 1505
 /gene="JNK3A2"
 68. 1462
 /gene="JNK3A2"
 /note="JNK protein kinase isoform that phosphorylates the transcription factor c-Jun on Ser-63 and Ser-73; protein kinase"
 /codon_start=1
 /product="JNK3 alpha2 protein kinase"
 /protein_id="AAC50604.1"
 /db_xref="GI:1463125"
 /translation="MSLHFLDYCSSEPTLDVKIAFCQGFQKQVDVYIAKHNNSSKVDNQFYEVEVDSTFTVLRKYQONKPIGSGAGQIVCAAYADVDRNVAIKLSRPFQNTAKRAVRELVLQMKCVNKHNIISLNVFTPOKTLIEFOVYVLMELADNLQVQIME LHERMSYLLYOMLCGIKLHSAIGIHRDLKPSNIIVKSDCTLIKIDFGARAGTGFNMTPYVTRVYRPAEYILMGYKENVKIDVSGCIGEMVNRHKLIFPGRIYDQMNVI EQLGTPCEPFMKLQPTVYNNYENRKYAGLTTPPKLPFSPSLFPADENHKLAKASQARD LSKMLVIDPARKISVDALQHPYINWWDPAVEAPPPQITDKQDEHEHTIEWKE LLYKEVMSNEEKTQNVKVGQPPSGAAVNSSESLPSSSVNDISSMSTDQTLASDPTLSLEASAGPLGCCR"

ORIGIN
 Query Match 10.3%; Score 82.8; DB 5; Length 1505;
 Best Local Similarity 97.7%; Pred. No. 3.9e-14;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GACCTGAGAGGAGGAGGCTGCTCTTACTACACCAATTTTACTCTTTCTTCTGAATTC 685
 |||||
 DB 1323 GCACCTGAGAGGAGGAGGCTGCTCTTACTACACCAATTTTACTCTTTCTTCTGAATTC 1264
 |||||
 QY 686 ATTACTTCTTGTAGATTAAGTTCTGT 711
 |||||
 DB 1263 ATTACTTCTTGTAGATTAAGTTCTTT 1238
 |||||

RESULT 17
 BC065516 1850 bp mRNA linear PRI 27-APR-2005
 LOCUS BC065516/c
 DEFINITION Homo sapiens mitogen-activated protein kinase 10, mRNA (cDNA clone IMAGE:5721954).
 ACCESSION BC065516
 VERSION BC065516.1 GI:41350833
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1850)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Fatcher, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,

McEwan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Maitra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1850)

JOURNAL NIH MGC Project
 PUBMED Direct Submission
 REFERENCE Submitted (26-JAN-2004) National Institutes of Health, Mammalian
 AUTHORS Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 TITLE NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 JOURNAL
 COMMENT
 REMARK
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Invitrogen
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisec.nih.gov/>
 Contact: nisc_mgc@nigri.nih.gov
 Akher, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Grant, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancirp, S., Thomas, P.J., Touchman, J.W., Tsurgenev, C., Vogt, J.L., Walker, M.A., Wecherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IPAK Plate: 139 Row: f Column: 4
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20586507.

FEATURES
 source
 1. 1850
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5721954"
 /tissue_type="Ovary, pooled from 3 adults"
 /clone_id="NIH MGC_125"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN
 Query Match 10.3%; Score 82.8; DB 5; Length 1850;
 Best Local Similarity 97.7%; Pred. No. 3.9e-14;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GACCTGAGAGGAGGAGGCTGCTCTTACTACACCAATTTTACTCTTTCTTCTGAATTC 685
 |||||
 DB 939 GCACCTGAGAGGAGGAGGCTGCTCTTACTACACCAATTTTACTCTTTCTTCTGAATTC 880
 |||||
 QY 686 ATTACTTCTTGTAGATTAAGTTCTGT 711
 |||||
 DB 879 ATTACTTCTTGTAGATTAAGTTCTTT 854
 |||||

RESULT 18
 AK091104/c
 LOCUS AK091104 2095 bp mRNA linear PRI 20-JAN-2006

```
DEFINITION Homo sapiens cDNA FLJ33765 fis, clone BRSSN2008125, highly similar
to MITOGEN-ACTIVATED PROTEIN KINASE 10 (EC 2.7.1.-).
ACCESSION AK091104
VERSION AK091104.1 GI:21749394
KEYWORDS Oligo capping, fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Oca, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekiue, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shitatori, A., Sudo, H., Hosoliri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Iehibashi, T., Yamashita, H.,
Hirooka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
Yosida, M., Houta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
Hara, H., Tanase, T. O., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A.,
Sasaki, N., Aocuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shibata, N., Sano, S., Moriya, S., Momiya, H., Sato, N., Takami, S.,
Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,
Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togoashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuno, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
JOURNAL
PUBMED
AUTHORS
REFERENCE
2 Iehibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S.,
Ono, Y., Houta, T., Hirooka, S., Murakawa, K., Takiguchi, S.,
Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M.,
Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Y.,
Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y.,
Sekiue, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 2095)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUN-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: f3j-cdnasequify.com, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
Source
1. 2095
Location/Qualifiers
/organism="Homo sapiens"

/mol_type="mrna"
/db_xref="taxon:9606"
/clone="BRSSN2008125"
/tissue_type="substantia nigra"
/clone_id="BRSSN2"
/note="cloning vector: pME185FL3"
ORIGIN
Query Match 10.3%; Score 82.8; DB 5; Length 2095;
Best Local Similarity 97.7%; Pred. No. 3.8e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
626 GRACCTGAAGGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTGAATTC 685
1208 GCACCTGAAGGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTGAATTC 1149
686 ATTACTCTCTGTAGATTAAGTTCTGT 711
1148 ATTACTCTCTGTAGATTAAGTTCTTT 1123
RESULT 19
CS206709/c 2211 bp DNA linear PAT 08-DEC-2005
LOCUS CS206709/c
DEFINITION Sequence 10 from Patent WO2005109001.
ACCESSION CS206709
VERSION CS206709.1 GI:83412264
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Spltlaels, K.F.
Patent: WO 2005109001-A 10 17-NOV-2005;
Galpagos Genomics N.V. (BE); Spltlaels, Koenraad Frederick F. (BE)
FEATURES
Source
1. 2211
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 2211;
Best Local Similarity 97.7%; Pred. No. 3.8e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
626 GRACCTGAAGGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTGAATTC 685
1323 GCACCTGAAGGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTGAATTC 1264
686 ATTACTCTCTGTAGATTAAGTTCTGT 711
1263 ATTACTCTCTGTAGATTAAGTTCTTT 1238
RESULT 20
BD078045/c 2366 bp DNA linear PAT 27-AUG-2002
LOCUS BD078045/c
DEFINITION JNK3-controller and method of using the same.
ACCESSION BD078045
VERSION BD078045.1 GI:22623648
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE
1 (bases 1 to 2366)
Davis, R.J., Flavell, R.A., Rakic, P., Whitmarsh, A.J., Kuan, C.Y. and
Yang, D.D.
JNK3-controller and method of using the same
Patent: JP 2001519146-A 2 23-OCT-2001;
UNIVERSITY OF MASSACHUSETTS
```

```

COMMENT
OS      Unidentified
PN      JP 2001519146-A/2
PD      23-OCT-2001
PF      05-OCT-1998 JP 2000514391
PR      03-OCT-1997 US 60/060995
PI      ROGER J DAVIS, RICHARD A FLAVELL, PASKO RAKIC, ALAN J WHITMARSH
PI      CHIA YIN KUAN,
PI      DERK DI YANG
PC      C12N15/09, A01K67/027, A61K31/711, A61K45/00, A61K48/00, A61P9/10,
PC      A61P23/00,
PC      A61P25/08, A61P25/14, A61P25/16, A61P25/28, C12N5/10, C12Q1/48, PC
C12Q1/48,
PC      G01N33/15, G01N33/50, C12N15/00, C12N5/00
CC      Strandedness: Double;
CC      Topology: Linear;
CC      JNK3-Controller and method of using the same
FH      Key
FT      source
FEATURES
source
1. .2366
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match
Best Local Similarity 97.7%; Score 82.8; DB 2; Length 2366;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626 GTAACCGAAGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
DB      1478 GCAACCGAAGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 1419
QY      686 ATTACTCTCTTGATAGTAAGTTCTGT 711
DB      1418 ATTACTCTCTTGATAGTAAGTTCTTT 1393

RESULT 21
LOCUS      AR716220 2367 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 3 from patent US 6943000.
ACCESSION AR716220
VERSION AR716220.1 GI:77364281
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2367)
AUTHORS Davis, R.J., Flavell, R.A., Rakic, P., Whitmarsh, A.J., Kuan, C.-Y. and Yang, D.D.
TITLE JNK3 modulators and methods of use
JOURNAL Patent: US 6943000-A 3 13-SEP-2005;
University of Massachusetts and Yale University, Boston, MA
FEATURES
source
1. .2367
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match
Best Local Similarity 97.7%; Score 82.8; DB 2; Length 2367;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626 GTAACCGAAGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 685
DB      1479 GCAACCGAAGAGGAGGCTGCTCTTACTACACCATTTTGTCTTTCTTCTGAATTC 1420
QY      686 ATTACTCTCTTGATAGTAAGTTCTGT 711
DB      1419 ATTACTCTCTTGATAGTAAGTTCTTT 1394

```

```

RESULT 22
LOCUS      BC051731/c
DEFINITION Homo sapiens mitogen-activated protein kinase 10, mRNA (CDNA clone
MGC:50974 IMAGE:4838495), complete cds.
ACCESSION BC051731
VERSION BC051731.1 GI:30704986
KEYWORDS
SOURCE MGC.
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 2494)
2494 bp mRNA linear PRI 06-OCT-2005
Homo sapiens mitogen-activated protein kinase 10, mRNA (CDNA clone
MGC:50974 IMAGE:4838495), complete cds.

REFERENCE
1 (bases 1 to 2494)
Faingold, E.A., Grouse, L.H., Derge, J.G.,
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diachenko, L., Marinina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramsen, R.D., Mialaby, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Wortley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchan, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalke, D.E.,
Scherer, A., Schein, J.E., Jones, S.J., and Matra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2494)

REFERENCE
AUTHORS NIH MGC Project
CONSRTM Direct Submission
TITLE Submitted (01-MAY-2003) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Email: cgapbs-remail.nih.gov
Contact: MGC help desk
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiroki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAC Plate: 90 Row: k Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 20986509.
FEATURES
source
1. .2494
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cclone="MGC:50974 IMAGE:4838495"
/cisue_type="Testis"
/cclone_1lb="NIH MGC_97"
/lab_host="DH10B"
/note="Vector: pBluecriptR"

```

```

gene
1. .2494
/ gene="MAPK10"
/ note="synonyms: p493f12, p54DSAPK, JNK3A, FLJ12059, JNK3"
/ db_xref="GeneID:5602"
/ db_xref="GeneID:6872"
/ db_xref="HGNC:6872"
/ db_xref="IMGT/GENE-DB:6872"
/ db_xref="MIM:602897"
768..1727
/ gene="MAPK10"
/ codon_start=1
/ product="MAPK10 protein"
/ protein_id="AAH51731.1"
/ db_xref="GI:71297339"
/ db_xref="GeneID:5602"
/ db_xref="HGNC:6872"
/ db_xref="IMGT/GENE-DB:6872"
/ db_xref="MIM:602897"
/ translation="MELMDANLCOVLEMDHERMSYLLYOMLCGILKHLHAGIIRH
LKPSNIVKSDCTLKIDFGIARTAGTSFMTPTVYVRYRABEVLIGMGYKENVDW
SVGCIEMEMIKGAVLPRGTDIDOMNKVIEOLGPGEPFKIKOPTVRNVERPKYA
GLTPPKLFPSPSLPRADSEHNKAKASQARDLSKMLYIDPAKRISVDALQPIYINWY
DPAVEAPPOIYDKOLDEREHTLEEKELIYKVMNSEKTNQGVKQSPSGAAV
NSESSELPSSSVNDISSMSDQTLASPTDSLEASAGPLCCCR"

ORIGIN
Query Match 10.3%; Score 82.8; DB 5; Length 2494;
Best Local Similarity 97.7%; Pred. No. 3.7e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTCTGGAATTC 685
DB 1588 GCACCTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTCTGGAATTC 1529
QY 686 ATTACTCTCTTGATAGATTCTGT 711
DB 1528 ATTACTCTCTTGATAGATTCTTT 1503

RESULT 23
AR454561/c
LOCUS AR454561
DEFINITION Sequence 34 from patent US 6682888.
ACCESSION AR454561
VERSION AR454561.1 GI:42688030
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2677)
AUTHORS Loring,J.F., Tingley,D.W. and Edwards,C.M.
TITLE Genes expressed in Alzheimer's disease
JOURNAL Patent: US 6682888-A 34 27-JAN-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
source
1..2677
/organism="Unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 2677;
Best Local Similarity 97.7%; Pred. No. 3.7e-14;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTTTTACTACACCAATTTTACTCTTCTGGAATTC 685
DB 1795 GCACCTGAAGAGAGAGGCTGCTTTTACTACACCAATTTTACTCTTCTGGAATTC 1736
QY 686 ATTACTCTCTTGATAGATTCTGT 711
DB 1735 ATTACTCTCTTGATAGATTCTTT 1710

RESULT 24

```

```

BC022492/c
LOCUS BC022492
DEFINITION 2678 bp mRNA linear PRI 14-OCT-2004
Homo sapiens mitogen-activated protein kinase 10, mRNA (cDNA clone
IMAGE:4792970).
BC022492
ACCESSION BC022492
VERSION BC022492.1 GI:18490289
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 2678)
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heish,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,T.E., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Uedin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
Mckernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huiyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Schevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schultz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Sklarska,V., Smallus,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2678)
REFERENCE
AUTHORS Director MGC Project.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@pax11.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAX Plate: 32 Row: b Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 20986504.
location/Qualifiers
1..2678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4792970"
/tissue_type="Brain, hypothalamus"
/clone_lib="NIH MGC_96"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN

```

Query Match 10.3%; Score 82.8; DB 5; Length 2678;
 Best Local Similarity 97.7%; Pred. No. 3.7e-14;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 685
 |
 DB 1775 GCACCTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 1716
 |
 QY 686 ATTACTCTCTGTAGATAGTCTTCTGT 711
 |
 DB 1715 ATTACTCTCTGTAGATAGTCTTCTT 1690
 |

RESULT 25
 BC035057/c 2690 bp mRNA linear PRI 03-AUG-2005
 LOCUS Homo sapiens mitogen-activated protein kinase 10, mRNA (cDNA clone
 DEFINITION MGC:41877 IMAGE:5261221), complete cds.
 ACCESSION BC035057
 VERSION BC035057.1 GI:71297045
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 1 (bases 1 to 2690)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettlemen, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2690)

JOURNAL
 PUBMED
 REFERENCE
 2 (bases 1 to 2690)

CONSRM
 TITLE
 NIH MGC Project
 Direct Submission
 Submitted (31-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2550, USA.
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shizaki
 Tohtiyuki and Piero Carninci (RIKEN)
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansystemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettlemen, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

REMARK
 COMMENT
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
 Series: IRAK Plate: 73 Row: d Column: 6
 This clone was selected for full length sequencing because it

FEATURES
 source
 passed the following selection criteria: matched mRNA gi: 20986509.
 Location/Qualifiers
 1..2690
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:41877 IMAGE:5261221"
 /issue_type="Brain, hippocampus"
 /clone_1ib="NIH MGC_95"
 /lab_host="DH10B"
 /note="Vector: pBluescript"

gene
 1..2690
 /gene="MAPK10"
 /note="synonyms: p493f12, p54bsAPK, JNK3A, FLJ12099, JNK3"
 /db_xref="GeneID:5602"
 /db_xref="MIM:602897"
 532..1926
 /gene="MAPK10"
 /codon_start=1
 /product="MAPK10 protein"
 /protein_id="AAH35057.1"
 /db_xref="GI:71297046"
 /db_xref="GeneID:5602"
 /db_xref="MIM:602897"
 /translation="MSLRLFLVYCSBPTLDVKIAFCGDFKQDVSVIAKHVMSKSV
 DNPQISVGVGSTFVTLKRYQNLKRGISGAGQIVCAADYALDRVALIKLSRPQNO
 THAKAYRELVLAMKVNHNKIIISLNVFTPQKTEEFQDYLVMELMDANLCQVOME
 LDHMSKSYLLVQMLCGIHLHSAGIHRDLKRSNTVVSDDTLKILDFGLARTAGTSF
 MNTPEVVRYPAPVILMGVYKENVDSVGCINGEMVNRHILPFGDYIDQWKKVI
 BOLGPECPKPKLOPTRVYVKNPKYAGLTFPLPDSLPADSEHNKLKASQAD
 LLSKVLVDPKARISVDALQHPRIYNNVDAEVAEAPPOIYDKGLDEEHKLEIEME
 LIYKWNMSERTKRGVYKQSPBGAIVNSSESLPSSSVNDISMSIDQTLASDSD
 SLEASAPLGGCR"

CDS
 1..2690
 /gene="MAPK10"
 /note="synonyms: p493f12, p54bsAPK, JNK3A, FLJ12099, JNK3"
 /db_xref="GeneID:5602"
 /db_xref="MIM:602897"
 532..1926
 /gene="MAPK10"
 /codon_start=1
 /product="MAPK10 protein"
 /protein_id="AAH35057.1"
 /db_xref="GI:71297046"
 /db_xref="GeneID:5602"
 /db_xref="MIM:602897"
 /translation="MSLRLFLVYCSBPTLDVKIAFCGDFKQDVSVIAKHVMSKSV
 DNPQISVGVGSTFVTLKRYQNLKRGISGAGQIVCAADYALDRVALIKLSRPQNO
 THAKAYRELVLAMKVNHNKIIISLNVFTPQKTEEFQDYLVMELMDANLCQVOME
 LDHMSKSYLLVQMLCGIHLHSAGIHRDLKRSNTVVSDDTLKILDFGLARTAGTSF
 MNTPEVVRYPAPVILMGVYKENVDSVGCINGEMVNRHILPFGDYIDQWKKVI
 BOLGPECPKPKLOPTRVYVKNPKYAGLTFPLPDSLPADSEHNKLKASQAD
 LLSKVLVDPKARISVDALQHPRIYNNVDAEVAEAPPOIYDKGLDEEHKLEIEME
 LIYKWNMSERTKRGVYKQSPBGAIVNSSESLPSSSVNDISMSIDQTLASDSD
 SLEASAPLGGCR"

ORIGIN
 Query Match 10.3%; Score 82.8; DB 5; Length 2690;
 Best Local Similarity 97.7%; Pred. No. 3.7e-14;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 685
 |
 DB 1787 GCACCTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTCTTCTTCTGAAATTC 1728
 |

QY 686 ATTACTCTCTGTAGATAGTCTTCTGT 711
 |
 DB 1727 ATTACTCTCTGTAGATAGTCTTCTT 1702
 |

RESULT 26
 CS206710/c 2698 bp DNA linear PAT 08-DEC-2005
 LOCUS CS206710 Sequence 11 from Patent WO2005109001.
 DEFINITION CS206710
 ACCESSION CS206710
 VERSION CS206710.1 GI:83412265
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 1
 Splittael, K.F.
 Patents: WO 2005109001-A 11 17-NOV-2005;
 Galapagos Genomics N.V. (BE); Splittael, Koenraad Frederick F. (BE)
 location/Qualifiers
 1..2698
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
 source
 passed the following selection criteria: matched mRNA gi: 20986509.
 Location/Qualifiers
 1..2698
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 10.3%; Score 82.8; DB 2; Length 2698;
 Best Local Similarity 97.7%; Pred. No. 3.7e-14;

Matches	84	Conservative	0	Mismatches	2	Indels	0	Gaps	0	
QY	626	GTACCTGAAGAGGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC	685	1810	GCACCTGAAGAGGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC	1751				
Db	686	ATTACTCTCTTGATAGTACTGCTGT	711	1750	ATTACTCTCTTGATAGTACTGCTTT	1725				
RESULT 27	AK124791	3081 bp	mRNA	linear	PRI 20-JAN-2006					
LOCUS	AK124791/c	Homo sapiens cDNA FLJ42801 fis, clone BRCAN2001223, highly similar								
DEFINITION	TO MITOGEN-ACTIVATED PROTEIN KINASE 10 (EC 2.7.1.-).									
ACCESSION	AK124791	GI:34530673								
VERSION	AK124791.1	GI:34530673								
KEYWORDS	oligo capping; fis (full insert sequence).									
REVISIONS	Homo sapiens (human)									
SOURCE	Homo sapiens									
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.									
REFERENCE	1	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Makamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oabayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsura, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirooka, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Houtua, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T. O., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takuchi, K., Arita, M., Imose, N., Mueashino, K., Yuyki, H., Oshima, A., Sasaki, N., Aocuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiraio, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.								
TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs									
JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)									
PUBMED	14702039									
REFERENCE	2	Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hiro, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Makamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.								
TITLE	Unpublished									
JOURNAL	3 (bases 1 to 3081)									
PUBMED	Isogai, T. and Yamamoto, J.									
REFERENCE	Direct Submission									
AUTHORS	Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,									
JOURNAL										

COMMENT	Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: flj-cdna@lifely.com, Tel:81-438-52-3975, Fax:81-438-52-3986) NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) (supported by Japan Key Technology Center etc.); 5' - 3' end one pass sequencing: RAB, HRI and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.
FEATURES	Location/Qualifiers
source	1..3081
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="BRCAN2001223"
	/tissue_type="caudate nucleus"
	/clone_id="BRCAN2"
	/note="cloning vector: pME185FL3"
ORIGIN	
Query Match	10.3%; Score 82.8; DB 5; Length 3081;
Best Local Similarity	97.7%; Pred. No. 3.7e-14;
Matches	84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC 685
Db	2194 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTGCTTTCTTGCAATTC 2135
QY	686 ATTACTCTCTTGATAGTACTGCTGT 711
Db	2134 ATTACTCTCTTGATAGTACTGCTGT 2109
RESULT 28	AY888567
LOCUS	AY888567/c
DEFINITION	Synthetic construct Homo sapiens clone FHL17970.01X
ACCESSION	AY888567
VERSION	AY888567.1 GI:61358131
KEYWORDS	Human ORF project.
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1 (bases 1 to 1269)
AUTHORS	Hines, B., Rolfs, A., Jepsen, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.
TITLE	Cloning of human full-length CDS in Creator (TM) recombinational vector system
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1269)
AUTHORS	Hines, B., Rolfs, A., Jepsen, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.
JOURNAL	Direct Submission
COMMENT	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD in-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.
FEATURES	Location/Qualifiers
source	1..1269
	/organism="synthetic construct"
	/mol_type="mRNA"

/db_xref="taxon:32630"
/clone="FLH117970.01X"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
1..1269
/gene="MAPK10"
1..1269
/gene="MAPK10"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/db_xref="GI:61358132"
/protein_id="AAK41509.1"
/translation="MSLHFLYLCSEPTLDVKIAFCGQFQKQDVSYIAKHNNKSKV
DNOFYSVEVDSTFTVLKRYONLKRIGSGAGQIVCAAYADVDNRVAIKLSRPNQ
THAKAYRELVLMKCVNHNKIIISLVNFTPQTEEPDYVLYMELMDANLCQVIME
LDHERMSYLLYOMLGGIKHLSAGIIRHDLKPSNIVVSDCTLKIDPGLARTAGTSF
MMTPYVTVRYRPAPEVILGMGKENVDISVGCINGEMWRHKLIPGRDYIDQMNKI
EOLGTCPEPMKQLOPTVRNRYENRKYAGLTFPKLPDLSLPADSEHNKLKASQARD
LISKMLVIDPAKRISVDALQHPYINWYDPAVEAPPPQIYDKQLDEREHTIEWKE
LYKEVMNSEKTKNGVVKGPSAQQVQO"

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 1193

Db 690 CTTCCTTGATGATAGTTCTGT 711
1192 CTTCCTTGATGATAGTTCTTT 1171

RESULT 29
AY890997/c 1269 bp mRNA linear SYN 21-MAR-2005
LOCUS Synthetic construct Homo sapiens clone FLH020610.01L
DEFINITION mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.
ACCESSION AY890997
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1269)
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
TITLE Cloning of human full-length CDS in Creator (TM) recombinational
vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1269)
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
TITLE Direct SubMISSION
JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular
REFERENCE Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
AUTHORS Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). The CDS has been directionally cloned using
BD in-Fusion (TM) cloning system between the SalI and HindIII sites
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
after SalI site and before 'ATG' to provide Kozak consensus
sequence; 'GG' after last codon and before HindIII site to maintain
reading frame. Each clone is clonally isolated and full-length
sequence-verified.

FEATURES
source Location/Qualifiers
1..1269
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="FLH020610.01L"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
1..1269
/gene="MAPK10"
1..1269
/gene="MAPK10"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AAK42931.1"
/db_xref="GI:61366953"
/translation="MSLHFLYLCSEPTLDVKIAFCGQFQKQDVSYIAKHNNKSKV
DNOFYSVEVDSTFTVLKRYONLKRIGSGAGQIVCAAYADVDNRVAIKLSRPNQ
THAKAYRELVLMKCVNHNKIIISLVNFTPQTEEPDYVLYMELMDANLCQVIME
LDHERMSYLLYOMLGGIKHLSAGIIRHDLKPSNIVVSDCTLKIDPGLARTAGTSF
MMTPYVTVRYRPAPEVILGMGKENVDISVGCINGEMWRHKLIPGRDYIDQMNKI
EOLGTCPEPMKQLOPTVRNRYENRKYAGLTFPKLPDLSLPADSEHNKLKASQARD
LISKMLVIDPAKRISVDALQHPYINWYDPAVEAPPPQIYDKQLDEREHTIEWKE
LYKEVMNSEKTKNGVVKGPSAQQVQO"

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 1193

Db 690 CTTCCTTGATGATAGTTCTGT 711
1192 CTTCCTTGATGATAGTTCTTT 1171

RESULT 30
AY891216/c 1269 bp mRNA linear SYN 21-MAR-2005
LOCUS Synthetic construct Homo sapiens clone FLH117966.01L
DEFINITION mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.
ACCESSION AY891216
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1269)
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
TITLE Cloning of human full-length CDS in Creator (TM) recombinational
vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1269)
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
TITLE Direct SubMISSION
JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular
REFERENCE Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
AUTHORS Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). The CDS has been directionally cloned using
BD in-Fusion (TM) cloning system between the SalI and HindIII sites
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'

after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.

FEATURES

source

Location/Qualifiers

1..1269

/organism="synthetic construct"

/mol_type="mRNA"

/db_xref="taxon:32630"

/clone="FLH117965.01X"

/lab_host="Escherichia coli DH5alpha T1 resistant"

/note="derived from Homo sapiens first strand cDNA library from placenta and brain"

1..1269

/gene="MAPK10"

gene

1..1269

CDS

1..1269

/gene="MAPK10"

/codon_start=1

/transl_table=11

/product="mitogen-activated protein kinase 10"

/protein_id="AA33143.1"

/db_xref="GI:61368268"

/translation="MSLHFLVYCSPTLDVKIAFCQGFQKQDVSYIAKYNNSKSKV
DNQFVSVEGDSFTVLKRYQNLKPIGSGAQGVCAVDAVLDNRVAIKLSRFPQNO
THAKAYRELVLAKCVNHNKIIISLNVFPQTLFEPDQVYLVMELMDANLCQVOME
LDHERMSYLLYOMLCGKHLHSGIITHDLKPSNIVYKSDCTLKILDFGLARAGTSF
MMTPYVTRRYRADEVILGKGVKENDIVSGCINGEMVRHKLIFPGROYIDQNNKVI
EOLGTPCEPFMKLOPTVRYNRYENRKYAGLTFPPLFPDSEHNKLSKQARD
LISKRLVIDPAKRISVDALQHPYINWVDPAVEAPPQIYDKOLDEREHTIEWKE
LIVKWNSEKTKNGVVGKQSPSAQVOQL"

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGGAATTCATTA 689

DB 1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGGAATTCATTA 1193

QY 690 CTTCCCTTGAGATAGTCTGT 711

DB 1192 CTTCCCTTGAGATAGTCTTT 1171

RESULT 31
AY893302 1269 bp mRNA linear SYN 16-MAR-2005
LOCUS AY893302

DEFINITION Synthetic construct Homo sapiens clone FLH057665.01X

mitogen-activated protein kinase 10 (MAPK10) mRNA, complete cds.

ACCESSION AY893302.1 GI:60815280

VERSION Human ORF Project.

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 1269)

AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,

Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.

TITLE Cloning of human full-length CDS FLEXGene in

Gateway (TM) recombinational vector system

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1269)

AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,

Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.

TITLE Direct Submission

JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular

Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,

Cambridge, MA 02141, USA

COMMENT This CDS clone is a part of a collection of human full-length

expression clones generated by Harvard Institute of Proteomics.

This ORF clone has been cloned with normalized stop-codon. AtC

recombination sites have been added to either end of the ORF and

directionally cloned using the Gateway cloning system into pDONR
201. Additional sequences in the clone: 'ACC' before the 'ATG'
(corresponding to ribosomal binding site and Kozak consensus
sequences). Each clone is clonally isolated and full-length
sequence-verified.

FEATURES

source

Location/Qualifiers

1..1269

/organism="synthetic construct"

/mol_type="mRNA"

/db_xref="taxon:32630"

/clone="FLH057665.01X"

/lab_host="Escherichia coli DH5alpha T1 resistant"

/note="derived from Homo sapiens first strand cDNA library from placenta and brain"

1..1269

/gene="MAPK10"

gene

1..1269

CDS

1..1269

/gene="MAPK10"

/codon_start=1

/transl_table=11

/product="mitogen-activated protein kinase 10"

/protein_id="AA33639.1"

/db_xref="GI:60815281"

/translation="MSLHFLVYCSPTLDVKIAFCQGFQKQDVSYIAKYNNSKSKV
DNQFVSVEGDSFTVLKRYQNLKPIGSGAQGVCAVDAVLDNRVAIKLSRFPQNO
THAKAYRELVLAKCVNHNKIIISLNVFPQTLFEPDQVYLVMELMDANLCQVOME
LDHERMSYLLYOMLCGKHLHSGIITHDLKPSNIVYKSDCTLKILDFGLARAGTSF
MMTPYVTRRYRADEVILGKGVKENDIVSGCINGEMVRHKLIFPGROYIDQNNKVI
EOLGTPCEPFMKLOPTVRYNRYENRKYAGLTFPPLFPDSEHNKLSKQARD
LISKRLVIDPAKRISVDALQHPYINWVDPAVEAPPQIYDKOLDEREHTIEWKE
LIVKWNSEKTKNGVVGKQSPSAQVOQL"

ORIGIN

Query Match 10.1%; Score 80.4; DB 8; Length 1269;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGGAATTCATTA 689

DB 1252 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTGGAATTCATTA 1193

QY 690 CTTCCCTTGAGATAGTCTGT 711

DB 1192 CTTCCCTTGAGATAGTCTTT 1171

RESULT 32
AY893752 1269 bp mRNA linear SYN 16-MAR-2005
LOCUS AY893752

DEFINITION Synthetic construct Homo sapiens clone FLH057664.01X

mitogen-activated protein kinase 10 (MAPK10) mRNA, partial cds.

ACCESSION AY893752.1 GI:60827196

VERSION Human ORF Project.

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 1269)

AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,

Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.

TITLE Cloning of human full-length CDS FLEXGene in

Gateway (TM) recombinational vector system

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1269)

AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,

Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.

TITLE Direct Submission

JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular

Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,

Cambridge, MA 02141, USA

COMMENT This CDS clone is a part of a collection of human full-length

expression clones generated by Harvard Institute of Proteomics.

This ORF clone has been cloned without stop-codon (to allow fusion

with C-terminal tag). After recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.

FEATURES

source

1..1269
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="FLH057664.01L"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library from placenta and brain"
1..>1269
/gene="MAPK10"
1..>1269
/gene="MAPK10"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AA36789.1"
/db_xref="GI:60827197"
/translation="MSLHRYCYSEPTLDVKIAFCQGFQKQVDVSYIAHYNMSKSV
DNQFVSEVGDSTFTVLRKYONLKPISGAGQIVCAAYDAVDNRVAIKLSRPFQNO
THAKRAYRELVLNKKCVNHNIIISLVNFPQKLEEFQDYLVMELMDANLCOVOME
LDHERMSYLLYOMLCGIKHLSAGIIRDLKPSNIVVKSCTLKILDFGLATAGTSF
MNTPTVYVRYAPREVILGMYKENVDIMSGCENGMVNRHKLIPGRDIADOWNKVI
EOLGTPCEPFMKLOPTVRYENRPNKAGLTFPDLSPDSEHNKLLKASQARD
LISKMLVIDPAKRISVDALQHPYINWVDPAVEVAPPOIYDKOLDEREHTIEWKE
LIYKVMNSEKTRNGVVKQSPSAVOOD"

ORIGIN

Query Match

Best Local Similarity 98.8%; Pred. No. 2.2e-13; Length 1269;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTCATTA 669
DB 1252 CTGAAGAGAGAGGCTGCTCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTCATTA 1193
QY 690 CTTCCTTGTAGTAAGTCTGT 711
DB 1192 CTTCCTTGTAGTAAGTCTTT 1171

RESULT 33

BT019710/c

LOCUS BT019710 1269 bp mRNA linear SYN 28-OCT-2004
DEFINITION Synthetic construct Homo sapiens mitogen-activated protein kinase
10 mRNA, partial cds.
BT019710
BT019710.1 GI:54696287
FLI CDNA.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 1269)
Kandina, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
Kandina, M., and Farmer, J., Morelta, D., Kelley, T., Labaer, J., Lin, Y.,
Phelan, M., and Farmer, J.

TITLE
Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector

JOURNAL
REFERENCE
2 (bases 1 to 1269)
Kandina, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
Kandina, M., and Farmer, J., Morelta, D., Kelley, T., Labaer, J., Lin, Y.,
Phelan, M., and Farmer, J.

TITLE
Direct Submission
JOURNAL
Submitted (28-OCT-2004) BD Biosciences Clontech, 1020 East Meadow
circle, Palo Alto, California 94303, USA
COMMENT
This CDS clone is a part of a collection of human full length

expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDONR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: <http://bioinfo.clontech.com/orfclones>.

FEATURES

source

1..1269
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="GH01307L1.0"
/clone_1lb="BD Creator(TM) CDS Library derived from MGC collection"
/lab_host="DH5alpha T1 resistant"
/note="vector: pDONR-Dual"
1..>1269
/note="Mutations: 1268:Stop->L"
/codon_start=1
/transl_table=11
/product="mitogen-activated protein kinase 10"
/protein_id="AAV38516.1"
/db_xref="GI:54696288"
/translation="MSLHRYCYSEPTLDVKIAFCQGFQKQVDVSYIAHYNMSKSV
DNQFVSEVGDSTFTVLRKYONLKPISGAGQIVCAAYDAVDNRVAIKLSRPFQNO
THAKRAYRELVLNKKCVNHNIIISLVNFPQKLEEFQDYLVMELMDANLCOVOME
LDHERMSYLLYOMLCGIKHLSAGIIRDLKPSNIVVKSCTLKILDFGLATAGTSF
MNTPTVYVRYAPREVILGMYKENVDIMSGCENGMVNRHKLIPGRDIADOWNKVI
EOLGTPCEPFMKLOPTVRYENRPNKAGLTFPDLSPDSEHNKLLKASQARD
LISKMLVIDPAKRISVDALQHPYINWVDPAVEVAPPOIYDKOLDEREHTIEWKE
LIYKVMNSEKTRNGVVKQSPSAVOOOL"

ORIGIN

Query Match

Best Local Similarity 98.8%; Pred. No. 2.2e-13; Length 1269;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTCATTA 669
DB 1252 CTGAAGAGAGAGGCTGCTCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTCATTA 1193
QY 690 CTTCCTTGTAGTAAGTCTGT 711
DB 1192 CTTCCTTGTAGTAAGTCTTT 1171

RESULT 34

BD249786/c

LOCUS BD249786 1306 bp DNA linear PAT 17-JUL-2003
DEFINITION Polypeptides derived from JNK3.
BD249786
BD249786.1 GI:33059556
KEYWORDS
JP 2002534982-A/22.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo

REFERENCE
1 (bases 1 to 1306)
Desanlis, F., Fournier, A., Maury, I. and Liu, O. Z.

TITLE
Polypeptides derived from JNK3
JOURNAL
Patent: JP 2002534982-A 22 22-OCT-2002;
AVENTIS PHARMA SA

COMMENT
OS Homo sapiens (human)
PN JP 2002534982-A/22
PD 22-OCT-2002
PF 19-JAN-2000 JP 2000594932
PR 20-JAN-1999 FR 99/00586, 26-FEB-1999 US 60/122175 PI
FRANCINE DESANLIS, ALAIN FOURNIER, ISABELLE MAURY, QING ZHOU LIU PC
C12N15/09, A61K39/395, A61K45/00, A61P7/10, A61P9/00, A61P25/00, PC

A61P25/14,
PC A61P25/16,A61P25/28,C07K16/40,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12N9/12
PC C12Q1/02,C12Q1/48,C12N15/00,C12N5/00
CC Polypeptides derived from JNK3
FH Key Location/Qualifiers
FT CDS (142)..(1293).
Location/Qualifiers
1..1306
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 1306;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGATTCATTA 689
DB 1279 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGATTCATTA 1220
QY 690 CTTCCTTTGATGATTAAGTTCTGT 711
DB 1219 CTTCCTTTGATGATTAAGTTCTTT 1198
RESULT 35
LOCUS AR430629/c 1306 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 22 from patent US 6649388.
ACCESSION AR430629
VERSION AR430629.1 GI:40191470
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1306)
AUTHORS Fournier,A., Maury,I., Zhou-Liu,Q. and Desanlis-Cremont,F.
TITLE Polypeptides derived from JNK3
JOURNAL Patent: US 6649388-A 22 18-NOV-2003;
Aventis Pharma S.A.; Antony;
FRX;
FEATURES
source Location/Qualifiers
1..1306
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 1306;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGATTCATTA 689
DB 1279 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGATTCATTA 1220
QY 690 CTTCCTTTGATGATTAAGTTCTGT 711
DB 1219 CTTCCTTTGATGATTAAGTTCTTT 1198
RESULT 36
LOCUS AX027293/c 1306 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 22 from Patent WO0043524.
ACCESSION AX027293
VERSION AX027293.1 GI:10188269
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
REFERENCE 1
AUTHORS Desanlis,F., Zhou-Liu,Q., Fournier,A. and Maury,I.
TITLE Polypeptides derived from jnk3
JOURNAL Patent: WO 0043524-A 22 27-JUL-2000;
AVENTIS PHARMA SA (FR) ; DESANLIS FRANCINE (FR) ; ZHOU LIU QING (FR) ; FOURNIER ALAIN (FR) ; MAURY ISABELLE (FR)
Location/Qualifiers
1..1306
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
142..1296
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC09125.1"
/db_xref="GI:10188270"
/translation="MSKSKVDNQFYSVEVGDSTFTVLRKYNLKPIGSGAGQIVCAAY
DAVLDRNVALIKLSRPNQTHAKRAYRELVLKMCVHNKNTISLNVFPQKLEPQ
DYLVNLMELDANLCVYIQMELDHERSYLLYQMLCGIKLHSGITTHRDLPKSNIVYK
SDCTKLIDFGRLRTAGISFWMTPVIVITRYABVILDMGKVENVDIVSGCIMGSM
VRRKILFPGRDYIDQWNVIEQLGTPCPEPMKQLQPTVNVYENRKYAGLTPPKLFP
DSLFPADSEHNKLKASQARDLISKMLVIDPAKRIQVDALQHPYIIVWYDPAVEAEP
POYKQDLDERHTIEWKELIYKEVWNSSEKTKNGVVGQPSAQQVOO"
ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 1306;
Best Local Similarity 98.8%; Pred. No. 2.2e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGATTCATTA 689
DB 1279 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGATTCATTA 1220
QY 690 CTTCCTTTGATGATTAAGTTCTGT 711
DB 1219 CTTCCTTTGATGATTAAGTTCTTT 1198
RESULT 37
LOCUS BD078046/c 1773 bp DNA linear PAT 27-AUG-2002
DEFINITION JNK3-controller and method of using the same.
ACCESSION BD078046
VERSION BD078046.1 GI:22623649
KEYWORDS JP 2001519146-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1773)
AUTHORS Davis,R.J., Flavell,R.A., Rakic,P., Whitmarsh,A.J., Kuan,C.Y. and Yang,D.D.
TITLE JNK3-controller and method of using the same
JOURNAL Patent: JP 2001519146-A 3 23-OCT-2001;
UNIVERSITY OF MASSACHUSETTS
COMMENT OS Unidentified
PN JP 2001519146-A/3
PD 23-OCT-2001
PF 05-OCT-1998 JP 2000514991
PR 03-OCT-1997 US 60/060995
PI ROGER J DAVIS, RICHARD A FLAVELL, PASKO RAKIC, ALAN J WHITMARSH
PI CHIA YIN KUAN,
PI DERK DI YANG
PC C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
PC A61P21/00,
PC A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C12Q1/48, PC
C12Q1/68,
PC GOIN3/15,GOIN3/50,C12N5/00,C12N5/00
CC Strandedness: Double;
CC Topology: Linear;
CC JNK3-controller and method of using the same
FH Key Location/Qualifiers
1..1773

```

FEATURES      University of Massachusetts and Yale University; Boston, MA
SOURCE        location/Qualifiers
              1. .1773
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN

```

Query Match	10.1%	Score 80.4	DB 2	Length 1773
Best Local Similarity	98.8%	Pred. No. 2,1e-11		
Matches 81, Conservative	0	Mismatches 1	Indels 0	Gaps 0

Db 1343 CTGAGAGGAGAGGCTGCTCTTTACTACACCAATTTTGTCTTTCTTGAAATTCATTA 1284

Db 1283 CTTCTGTAGATAGTCTTT 1262

RESULT 40	AX377859/c	LOCUS	AX377859	1773 bp	DNA	linear	PAT 18-MAR-2002
DEFINITION			Sequence 54 from Patent WO0212358.				
ACCESSION			AX377859				
VERSION			AX377859.1	GI:19573950			
KEYWORDS							
SOURCE							
ORGANISM							
			Homo sapiens (human)				
			Homo sapiens				
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

REFERENCE	1
AUTHORS	Gillen,C., Wetzels,I., Wnendt,S., Wehne,E. and Schaefer,M.K
TITLE	Screening method
JOURNAL	Patent: WO 0212338-A 54 14-FEB-2002;
FEATURES	Gruenenthal GmbH (DE)
	Location/Qualifiers

```

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```

Query Match	10.1%	Score 80.4	DB 2	Length 1773
Best Local Similarity	98.8%	Pred. No. 2.1e-13		
Matches 81	Conservative 0	Mismatches 1	Indels 0	Gaps 0

Qy	630	CTAAGAGAAAGGCTGCGCTTTACTACACACATTTTATGCTTTTCCTCGAATTCATTA	689
Db	1343	CTAAGAGAAAGGCTGCGCTTTACTACACCATTTTATGCTTTTCCTGAATTCATTA	1284
Qy	690	CTTCCTGTGATAGATTCGT	711
Db	1283	CTTCCTGTGATAGATTCCTT	1262

RESULT 41	
HSU34820/c	HSU34820 1773 bp mRNA linear PRI 25-JUL-1996
LOCUS	HSU34820
DEFINITION	Human JNK3 alpha1 protein kinase (JNK3A1) mRNA, complete cds.
ACCESSION	U34820.
VERSION	U34820.1 GI:1463126
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiinae; Homo.
AUTHORS	1 (bases 1 to 1773) Gupta, S., Barrett, T., Whitmarsh, A.J., Cavanagh, J., Sluss, H.K., Derjard, B. and Davis, R.J.
TITLE	Selective interaction of JNK protein kinase isoforms with

transcription factors
 JOURNAL EMBL J. 15 (11), 2760-2770 (1996)
 PUBMED 8654373
 REFERENCE 2 (bases 1 to 1773)
 AUTHORS Davis, R.J.
 TITLE Direct Submission
 JOURNAL Submitted (25-AUG-1995) Roger J. Davis, Molecular Medicine, University of Massachusetts Medical School, 373 Plantation Street, Worcester, MA 01605, USA
 COMMENT Derijard, B. Cell 76, 1025-1037, 1994
 Stuss, H. K. Mol. Cell. Biol. 14, 8376-8384, 1994.
 FEATURES
 source
 1. 1773
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="brain"
 1. 1773
 /gene="JUNK3A1"
 92. 1360
 /gene="JUNK3A1"
 /note="JNK protein kinase isoform that phosphorylates the transcription factor C-Jun on Ser-63 and Ser-73"
 /codon_start=1
 /product="JNK3 alpha1 protein kinase"
 /protein_id="AAC50605.1"
 /db_xref="GI:11463127"
 /translation="MSLHFLYCYSEPTLDVKIAFCQGFQKQDVSYIARHNSKSKV
 DNPQYSEVSDSTFVLYKRYONLKPISGGQGIQVAYDAVLDNRVAIKKLSRPQNO
 THAKRAYRELVLMKCVNHKNIIISLNVFTPEQKLEFQDVLYMELMDNLCOVIME
 LDHERMSYLLQMLCGIKLHSGIIRHDLKPSNTIVYKSDCTIKILDPGLARTGSGF
 NMTPYVTVYRPAEYVILGKGYENVDISVGTIKEMEMRHKILFEGRPYIDQMNVI
 EQLGTCPERPKLQPTKRYVYENRKRIGLTFPKLPSPSLFADSEHNKLUASQARD
 LISKMLVIDPAKISVDALQHPYINWVDPAPVEAPPOIYDKQLDEREHTLEWKE
 LIYKEVMSBEKTRNGVXGQSPSPSAVQOQ"
 ORIGIN
 Query Match 10.1%; Score 80.4; DB 5; Length 1773;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGCGTCTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 689
 |||||
 DB 1343 CTGAAGAGAGAGCGTCTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 1284
 |||||
 QY 690 CTTCTGTAGATAAGTTCTGT 711
 |||||
 DB 1283 CTTCTGTAGATAAGTTCTTT 1262
 |||||
 RESULT 42
 CQ714411/c 2096 bp DNA linear PAT 03-FEB-2004
 LOCUS CQ714411
 DEFINITION Sequence 345 from Patent WO02068579.
 ACCESSION CQ714411
 VERSION CQ714411.1 GI:42275268
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 TITLE Kite, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 JOURNAL Patent: WO 02068579-A 345 06-SBP-2002;
 PE Corporation (NY) (US)
 FEATURES
 source
 1. 2096
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"

/db_xref="taxon:9606"
 ORIGIN
 Query Match 10.1%; Score 80.4; DB 2; Length 2096;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGCGTCTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 689
 |||||
 DB 1199 CTGAAGAGAGAGCGTCTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 1140
 |||||
 QY 690 CTTCTGTAGATAAGTTCTGT 711
 |||||
 DB 1139 CTTCTGTAGATAAGTTCTTT 1118
 |||||
 RESULT 43
 AR709626/c 2131 bp DNA linear PAT 21-SEP-2005
 LOCUS AR709626
 DEFINITION Sequence 87 from patent US 6936450.
 ACCESSION AR709626
 VERSION AR709626.1 GI:76000136
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2131)
 AUTHORS Levine, Z. and Bernstein, J.
 TITLE Variants of protein kinases
 JOURNAL Patent: US 6936450-A 87 30-AUG-2005;
 Compugen Ltd.; Tel Aviv;
 WO/;
 FEATURES
 source
 1. 2131
 /location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 10.1%; Score 80.4; DB 2; Length 2131;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGCGTCTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 689
 |||||
 DB 1225 CTGAAGAGAGAGCGTCTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 1166
 |||||
 QY 690 CTTCTGTAGATAAGTTCTGT 711
 |||||
 DB 1165 CTTCTGTAGATAAGTTCTTT 1144
 |||||
 RESULT 44
 CS206711/c 2155 bp DNA linear PAT 08-DEC-2005
 LOCUS CS206711/c
 DEFINITION Sequence 12 from Patent WO2005109001.
 ACCESSION CS206711
 VERSION CS206711.1 GI:83412266
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 Splittlaels, K.F.
 AUTHORS Splittlaels, K.F.
 TITLE Patent: WO 2005109001-A 12 17-NOV-2005;
 JOURNAL Galapagos Genomics N.V. (BE); Splittlaels, Koenraad Frederick F. (BE)
 FEATURES
 source
 1. 2155
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN

Query Match 10.1%; Score 80.4; DB 2; Length 2155;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 630 CTGAAGAGAAAGCGTGCCTTTACTACACCATTTTACTCTTCTTCTGAAATCATTA 689
 |||||
 Db 1258 CTGAAGAGAAAGCGTGCCTTTACTACACCATTTTACTCTTCTTCTGAAATCATTA 1199
 |||||

Y 690 CTTCCTTGATGATGATGCTTCTGT 711
 |||||
 Db 1198 CTTCCTTGATGATGATGCTTCTT 1177
 |||||

RESULT 45
 AK057723 2156 bp mRNA linear PRI 20-JAN-2006
 LOCUS AK057723/c Homo sapiens CDNA FLJ33161.f1s, clone UTERU2000517, highly similar
 DEFINITION to MITOGEN-ACTIVATED PROTEIN KINASE 10 (EC 2.7.1.-).

ACCESSION AK057723.1 GI:16553642
 VERSION AK057723.1
 KEYWORDS oligo capping; full insert sequence
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
 Wakamatsu, Y., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
 Sekine, M., Okeyashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
 Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
 Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
 Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
 Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
 Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
 Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
 Murakawa, K., Fujimori, K., Tanai, H., Kimura, M., Watanabe, M.,
 Hirooka, S., Chiba, Y., Ishida, S., Oono, Y., Takiguchi, S., Watanabe, S.,
 Hirotsu, M., Hoota, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
 Hara, H., Tanase, T. O., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
 Takeuchi, K., Arita, M., Imose, N., Musahino, K., Yuki, H., Oshima, A.,
 Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsumura, H., Ichihara, T.,
 Shibata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
 Tereshima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
 Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
 Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
 Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
 Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,
 Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
 Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
 Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
 Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaashi, T.,
 Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
 Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
 Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
 Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isegai, T. and Sugano, S.
 Complete sequencing and characterization of 21,243 full-length
 human cDNAs
 JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
 PubMed 14702039
 REFERENCE
 AUTHORS

TITLE Nagahari, K., Masuho, Y., Nagai, K. and Isegai, T.
 JOURNAL NEDO human CDNA sequencing project
 REFERENCE 3 (bases 1 to 2156)
 AUTHORS Isegai, T., Otsuki, T. and Sugiyama, T.
 JOURNAL Direct Submission
 COMMENT Submitted (24-Oct-2001) Takao Isegai, Helix Research Institute,
 Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail: filj-cdna@helix.com, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human CDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; CDNA full insert sequencing:
 Research Association for Biotechnology (RAB) (CDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5' - & 3' - end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: RAB and
 HRI.

FEATURES
 source location/Qualifiers
 1..2156
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UTERU2000517"
 /tissue_type="uterus"
 /clone_id="UTERU2"
 /note="Cloning vector: pME18SFL3"

ORIGIN
 Query Match 10.1%; Score 80.4; DB 5; Length 2156;
 Best Local Similarity 98.8%; Pred. No. 2.1e-13;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 630 CTGAAGAGAAAGCGTGCCTTTACTACACCATTTTACTCTTCTTCTGAAATCATTA 689
 |||||
 Db 1260 CTGAAGAGAAAGCGTGCCTTTACTACACCATTTTACTCTTCTTCTGAAATCATTA 1201
 |||||

Y 690 CTTCCTTGATGATGATGCTTCTGT 711
 |||||
 Db 1200 CTTCCTTGATGATGATGCTTCTT 1179
 |||||

RESULT 46
 BD078047/c
 LOCUS BD078047.1
 DEFINITION JNK3-controller and method of using the same.
 ACCESSION BD078047
 VERSION BD078047.1 GI:22623650
 KEYWORDS JP 2001519146-A/4.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.
 1 (bases 1 to 2372)
 Davis, R.J., Flavell, R.A., Rakic, P., Whitmarsh, A.J., Xuan, C.Y. and
 Yang, D.D.
 JNK3-controller and method of using the same
 Patent: JP 2001519146-A 4 23-OCT-2001;
 UNIVERSITY OF MASSACHUSETTS
 OS Unidentified
 PN JP 2001519146-A/4
 PD 23-OCT-2001
 PF 05-OCT-1998 JP 2000514991
 PR 03-OCT-1997 US 60/060995
 PI ROGER J DAVIS, RICHARD A FLAVELL, PASKO RAKIC, ALAN J WHITMARSH
 PI CHIA YIN XUAN,
 PI DERK DI YANG
 PC C12N15/09,A01K67/027,A61K31/711,A61K45/00,A61K48/00,A61P9/10,
 PC A61P21/00,
 PC A61P25/08,A61P25/14,A61P25/16,A61P25/28,C12N5/10,C12Q1/48, PC
 C12Q1/68,
 PC GOIN3/15,GOIN3/50,C12N15/00,C12N5/00
 CC Strandedness: Double;
 CC Topology: Linear;
 CC JNK3-controller and method of using the same

Db 1415 CTCCTGTGTAGATAGTCTTT 1394

RESULT 50

AR716222/c

AR716222

2372 bp

DNA

linear

PAT 07-OCT-2005

LOCUS

DEFINITION

Sequence 6 from patent US 6943000.

Accession

AR716222

GI:77364283

VERSION

AR716222.1

GI:77364283

KEYWORDS

Unknown.

Unknown.

SOURCE

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 2372)

Davis, R.J., Flavell, R.A., Rakic, P., Whitmarsh, A.J., Kuan, C.-Y. and Yang, D.D.

AUTHORS

JNK3 modulators and methods of use

Patent: US 6943000-A 6 13-SEP-2005;

University of Massachusetts and Yale University; Boston, MA

Location/Qualifiers

1. 2372

FEATURES

source

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 10.1%; Score 80.4; DB 2; Length 2372;

Best Local Similarity 98.8%; Pred. No. 2.1e-13;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1415 CTCCTGTGTAGATAGTCTTT 1394

QY

630 CTGAGGAGAGAGCTGTCTTACTACACCATTTTACTTCTTCTGATTCATTA 689

1475 CTGAGGAGAGAGCTGTCTTACTACACCATTTTACTTCTTCTGATTCATTA 1416

QY

690 CTCCTGTGTAGATAGTCTTT 711

1415 CTCCTGTGTAGATAGTCTTT 1394

Search completed: July 19, 2006, 20:10:46

Job time : 5076 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:38:55 ; Search time 650 Seconds
(without alignments)
8581.229 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800
Sequence: 1.acattctctaactctta.....caataatactgcttgatg 800

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

-Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

N_Geneseq_8:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004as:*

13: Geneseq2004bs:*

14: Geneseq2005s:*

15: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	798.4	99.8	76500	ADP45592 Human MAP
2	798.4	99.8	110950	ADP45592 Human MAP
3	463.4	57.9	823	ADY03500 Human mit
4	463.4	57.9	823	ADY03500 Human mit
5	82.8	10.3	1281	ABK50805 DNA encod
6	82.8	10.3	1422	AAA59380 DNA encod
7	82.8	10.3	1505	AAK37266 Nucleic a
8	82.8	10.3	1505	ABL88412 Pain regu
9	82.8	10.3	1505	ADL1626 Human cDN
10	82.8	10.3	1505	ADL1626 Human cDN
11	82.8	10.3	2211	ADSG83693 Human lym
12	82.8	10.3	2367	AAK37267 Seg ID No
13	82.8	10.3	2677	ADL1666 Human cDN
14	82.8	10.3	2677	ADL1666 Human cDN
15	82.8	10.3	2677	ADL1666 Human cDN
16	80.4	10.1	972	AAK37267 Human MAP
17	80.4	10.1	999	AAK37267 Human MAP
18	80.4	10.1	1111	AAK37267 Human MAP

C 19	80.4	10.1	1306	AAA59379 DNA encod
C 20	80.4	10.1	1773	ABL88411 Pain regu
C 21	80.4	10.1	1773	ABL88411 Pain regu
C 22	80.4	10.1	1872	ADSG8365 Human pro
C 23	80.4	10.1	2155	AAK37267 Human MAP
C 24	80.4	10.1	2372	AAK37267 Human MAP
C 25	80.4	10.1	2372	AAK37267 Human MAP
C 26	80.4	10.1	2372	AAK37267 Human MAP
C 27	80.4	10.1	2372	AAK37267 Human MAP
C 28	80.4	10.1	2372	AAK37267 Human MAP
C 29	80.4	10.1	2372	AAK37267 Human MAP
C 30	80.4	10.1	2372	AAK37267 Human MAP
C 31	80.4	10.1	2372	AAK37267 Human MAP
C 32	80.4	10.1	2372	AAK37267 Human MAP
C 33	80.4	10.1	2372	AAK37267 Human MAP
C 34	80.4	10.1	2372	AAK37267 Human MAP
C 35	80.4	10.1	2372	AAK37267 Human MAP
C 36	80.4	10.1	2372	AAK37267 Human MAP
C 37	80.4	10.1	2372	AAK37267 Human MAP
C 38	80.4	10.1	2372	AAK37267 Human MAP
C 39	80.4	10.1	2372	AAK37267 Human MAP
C 40	80.4	10.1	2372	AAK37267 Human MAP
C 41	80.4	10.1	2372	AAK37267 Human MAP
C 42	80.4	10.1	2372	AAK37267 Human MAP
C 43	80.4	10.1	2372	AAK37267 Human MAP
C 44	80.4	10.1	2372	AAK37267 Human MAP
C 45	80.4	10.1	2372	AAK37267 Human MAP
C 46	80.4	10.1	2372	AAK37267 Human MAP
C 47	80.4	10.1	2372	AAK37267 Human MAP
C 48	80.4	10.1	2372	AAK37267 Human MAP
C 49	80.4	10.1	2372	AAK37267 Human MAP
C 50	80.4	10.1	2372	AAK37267 Human MAP
C 51	80.4	10.1	2372	AAK37267 Human MAP
C 52	80.4	10.1	2372	AAK37267 Human MAP
C 53	80.4	10.1	2372	AAK37267 Human MAP
C 54	80.4	10.1	2372	AAK37267 Human MAP
C 55	80.4	10.1	2372	AAK37267 Human MAP
C 56	80.4	10.1	2372	AAK37267 Human MAP
C 57	80.4	10.1	2372	AAK37267 Human MAP
C 58	80.4	10.1	2372	AAK37267 Human MAP
C 59	80.4	10.1	2372	AAK37267 Human MAP
C 60	80.4	10.1	2372	AAK37267 Human MAP
C 61	80.4	10.1	2372	AAK37267 Human MAP
C 62	80.4	10.1	2372	AAK37267 Human MAP
C 63	80.4	10.1	2372	AAK37267 Human MAP
C 64	80.4	10.1	2372	AAK37267 Human MAP
C 65	80.4	10.1	2372	AAK37267 Human MAP
C 66	80.4	10.1	2372	AAK37267 Human MAP
C 67	80.4	10.1	2372	AAK37267 Human MAP
C 68	80.4	10.1	2372	AAK37267 Human MAP
C 69	80.4	10.1	2372	AAK37267 Human MAP
C 70	80.4	10.1	2372	AAK37267 Human MAP
C 71	80.4	10.1	2372	AAK37267 Human MAP
C 72	80.4	10.1	2372	AAK37267 Human MAP
C 73	80.4	10.1	2372	AAK37267 Human MAP
C 74	80.4	10.1	2372	AAK37267 Human MAP
C 75	80.4	10.1	2372	AAK37267 Human MAP
C 76	80.4	10.1	2372	AAK37267 Human MAP
C 77	80.4	10.1	2372	AAK37267 Human MAP
C 78	80.4	10.1	2372	AAK37267 Human MAP
C 79	80.4	10.1	2372	AAK37267 Human MAP
C 80	80.4	10.1	2372	AAK37267 Human MAP
C 81	80.4	10.1	2372	AAK37267 Human MAP
C 82	80.4	10.1	2372	AAK37267 Human MAP
C 83	80.4	10.1	2372	AAK37267 Human MAP
C 84	80.4	10.1	2372	AAK37267 Human MAP
C 85	80.4	10.1	2372	AAK37267 Human MAP
C 86	80.4	10.1	2372	AAK37267 Human MAP
C 87	80.4	10.1	2372	AAK37267 Human MAP
C 88	80.4	10.1	2372	AAK37267 Human MAP
C 89	80.4	10.1	2372	AAK37267 Human MAP
C 90	80.4	10.1	2372	AAK37267 Human MAP
C 91	80.4	10.1	2372	AAK37267 Human MAP

C 92	42	5.2	1.12	10	AD56.01	Ad56.01 DNA, sequen
C 93	42	5.2	1.18	2	AA085308	AA085308 UNK1 Onco
C 94	42	5.2	1.18	2	AA448625	AA448625 Human UNK
C 95	42	5.2	1.18	6	AA148612	AA148612 Human ins
C 96	42	5.2	1.18	6	ABK83865	ABK83865 Human CDN
C 97	42	5.2	1.18	9	ADA26307	ADA26307 CDNA enco
C 98	42	5.2	1.18	9	ACA62748	ACA62748 Human c-J
C 99	42	5.2	1.18	14	AD11.993	Adz11.993 Human Jun
C 100	42	5.2	1.18	14	AED33361	Aed33361 Human pro

ALIGNMENTS

RESULT	1
ID	ADP45592
ADP45592	standard; DNA; 76500 BP.
XX	
AC	ADP45592;
XX	
DT	26-AUG-2004 (first entry)
XX	
DE	Human MAP kinase MAPK10 (JNK3) gDNA.
XX	
KW	breast cancer; cytoskeletal; gene therapy; human; ds; gene; SNP;
KW	single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; JNK3A; p493F12;
KW	p54SAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;
KW	c-Jun N-terminal kinase 3; stress activated protein kinase beta;
KW	chromosome 4q22.1-q23.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	191
FT	/tag= a
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	1490
FT	/tag= b
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	3781
FT	/tag= c
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	3935
FT	/tag= d
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	4512
FT	/tag= e
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	7573
FT	/tag= f
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	8467
FT	/tag= g
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	9001
FT	/tag= h
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	9732
FT	/tag= i
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	13477
FT	/tag= j
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	13787
FT	/tag= k
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	13903
FT	/tag= l
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	14355
FT	/tag= m
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
FT	15053
FT	/standard_name= "Single nucleotide polymorphism (SNP)"

FT	/tag= n	"Single nucleotide polymorphism (SNP) "
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	15459	
FT	/tag= o	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	17762	
FT	/tag= p	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	19482	
FT	/tag= q	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	19631	
FT	/tag= r	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	22170	
FT	/tag= s	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	22688	
FT	/tag= t	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	22748	
FT	/tag= u	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	23376	
FT	/tag= v	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	23826	
FT	/tag= w	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	23868	
FT	/tag= x	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	24154	
FT	/tag= y	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	25972	
FT	/tag= z	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26057	
FT	/tag= aa	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26361	
FT	/tag= ab	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26599	
FT	/tag= ac	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26712	
FT	/tag= ad	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	26812	
FT	/tag= ae	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	27069	
FT	/tag= af	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	32421	
FT	/tag= ag	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	33557	
FT	/tag= ah	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	35127	
FT	/tag= ai	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	35222	
FT	/tag= aj	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	35999	
FT	/tag= ak	
FT	/standard_name=	"Single nucleotide polymorphism (SNP) "
FT	36424	
FT	/tag= al	


```
KM Jun N terminal kinase-3; MAPK10.
XX Homo sapiens.
OS
FH Key
FT Location/Qualifiers
FT 206
FT /+tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 1505
FT /+tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 3796
FT /+tag= c
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 3950
FT /+tag= d
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 4527
FT /+tag= e
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 7588
FT /+tag= f
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 8482
FT /+tag= g
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 9016
FT /+tag= h
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 9018
FT /+tag= i
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 9747
FT /+tag= j
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 12207
FT /+tag= k
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13040
FT /+tag= l
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13492
FT /+tag= m
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13802
FT /+tag= n
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 13918
FT /+tag= o
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 14153
FT /+tag= p
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 14370
FT /+tag= q
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 15068
FT /+tag= r
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 15474
FT /+tag= s
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 17117
FT /+tag= t
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 17777
FT /+tag= u
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 19497
FT /+tag= v
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 19646
FT /+tag= w
FT variation
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 21731
FT /+tag= x
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 22185
FT /+tag= y
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 22703
FT /+tag= z
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 22763
FT /+tag= aa
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 23391
FT /+tag= ab
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 23841
FT /+tag= ac
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 23883
FT /+tag= ad
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 24132
FT /+tag= ae
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 24169
FT /+tag= af
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 25987
FT /+tag= ag
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26072
FT /+tag= ah
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26376
FT /+tag= ai
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26514
FT /+tag= aj
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26727
FT /+tag= ak
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 26827
FT /+tag= al
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 27084
FT /+tag= am
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 30965
FT /+tag= an
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 32436
FT /+tag= ao
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 32821
FT /+tag= ap
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 32979
FT /+tag= aq
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 33572
FT /+tag= ar
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 35142
FT /+tag= as
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 35237
FT /+tag= at
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT 36014
FT /+tag= au
FT /standard_name= "Single nucleotide polymorphism (SNP)"
```



```

FT      variation      replace(36424,C).
FT      /*tag= av
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36439
FT      variation      /*tag= aw
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36838
FT      variation      /*tag= ax
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36889
FT      variation      /*tag= ay
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36839
FT      variation      /*tag= az
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36857
FT      variation      /*tag= ba
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36865
FT      variation      /*tag= bb
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      36885
FT      variation      /*tag= bc
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      38943
FT      variation      /*tag= bd
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39035
FT      variation      /*tag= be
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39046
FT      variation      /*tag= bf
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39218
FT      variation      /*tag= bg
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      39241
FT      variation      /*tag= bh
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
FT      40105
FT      variation      /*tag= bi
FT      /standard_name= "Single nucleotide polymorphism (SNP)"

Query Match      99.8%; Score 798.4; DB 14; Length 110950;
Best Local Similarity 99.9%; Pred. No. 2.9e-171;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ACATTTTCTAAACCTTTATAGTGTGAGACATAGGCTTAGGAAAAATATATAGCATT 60
DB      36016 ACATTTTCTAAACCTTTATAGTGTGAGACATAGGCTTAGGAAAAATATATAGCATT 36075
QY      61 AATAAGTAATGTGTCTCAAGCATACCTAAAGACATTAAGGATCAGTAAAAATAAT 120
DB      36076 AATAAGTAATGTGTCTCAAGCATACCTAAAGACATTAAGGATCAGTAAAAATAAT 36135
QY      121 ATGCACATTTGCTGTTAGATCTGTGCTGACCAAGAAAAATTTTCCAGCTGACCTT 180
DB      36136 ATGCACATTTGCTGTTAGATCTGTGCTGACCAAGAAAAATTTTCCAGCTGACCTT 36195
QY      181 AACCGAGCCCATCTGTGATAGTGTTCACATATGTGCATCAACCTTGAGAAAGATTC 240
DB      36196 AACCGAGCCCATCTGTGATAGTGTTCACATATGTGCATCAACCTTGAGAAAGATTC 36255
QY      241 AAACACTAAGATGAATGAGGAGAGAGGTAGCGGCTGAAAGATTACTGAGCTCCACATT 300
DB      36256 AAACACTAAGATGAATGAGGAGAGAGGTAGCGGCTGAAAGATTACTGAGCTCCACATT 36315
QY      301 GACTTGATGCTCAAAAGGCAATTATGCTGTAATTTTGAAGGCAACATTAACCTTTA 360
DB      36316 GACTTGATGCTCAAAAGGCAATTATGCTGTAATTTTGAAGGCAACATTAACCTTTA 36375
QY      361 GCCCATGTTAACTTTCTTCAGATTCATTAATTAATTTATGAAAAAGTTT 420
DB      36376 GCCCATGTTAACTTTCTTCAGATTCATTAATTAATTTATGAAAAAGTTT 36435
QY      421 TGTCTGTGATCATTTACCATCAAGATATGATGATCCACACTGAATATCAAAAGAA 480
DB      36436 TGTCTGTGATCATTTACCATCAAGATATGATGATCCACACTGAATATCAAAAGAA 36495
QY      481 ATPAAACTAATTCATTTATTAAGACACAAAGTGAATTTTGTGATGCTGCTTTAAG 540
DB      36496 ATPAAACTAATTCATTTATTAAGACACAAAGTGAATTTTGTGATGCTGCTTTAAG 36555
QY      541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACACAAGTACTAG 600
DB      36556 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTACACAAGTACTAG 36615
QY      601 TTTATGTTATTCACGAGAGTGAATCCTGAGAGAGAGAGGCTGCTTTTACTACACC 660
DB      36616 TTTATGTTATTCACGAGAGTGAATCCTGAGAGAGAGAGGCTGCTTTTACTACACC 36675
QY      661 ATTTTATGCTTTTCTTGCAATTCATTAATCCTGTTAGATTAAGTTGTTAAGAAACAG 720
DB      36676 ATTTTATGCTTTTCTTGCAATTCATTAATCCTGTTAGATTAAGTTGTTAAGAAACAG 36735
QY      721 CTGTGTTATTAAGAAAAAATAATTAATCCTTCATCAACAGGAAATTCATTACTTAATGC 780
DB      36736 CTGTGTTATTAAGAAAAAATAATTAATCCTTCATCAACAGGAAATTCATTACTTAATGC 36795
QY      781 CAATTAATTAAGTTTGAATG 800
DB      36796 CAATTAATTAAGTTTGAATG 36815

RESULT 3
ADY03500
ID      ADY03500 standard; DNA; 823 BP.
XX
XX      ADY03500;
AC
XX
XX      05-MAY-2005 (first entry)
DT
XX
XX      Human mitogen-activated protein kinase 10 SNP-containing gDNA MAPK10-AC.
DE
XX
XX      SNP detection; breast tumor; endocrine disease;
XX      gynecology and obstetrics; neoplasm; cytostatic; metastasis;
XX      gene therapy; RNA interference; chromosome 4; ds; SNP;
XX      single nucleotide polymorphism; mitogen-activated protein kinase 10;
XX      Jun N terminal kinase-3; MAPK10.
OS
XX
XX      Homo sapiens.
FH
XX
XX      Key      Location/Qualifiers
FT      variation      488
FT      /*tag= a
FT      /standard_name= "Single nucleotide polymorphism (SNP)"
PV      WO2005014846-A2.
XX
XX      17-FEB-2005.
PD
XX
XX      27-MAY-2004; 2004WO-US016939.
PF
XX
XX      24-JUL-2003; 2003US-0490234P.
PR      25-NOV-2003; 2003US-00723681.
PR      25-NOV-2003; 2003US-0525239P.
XX
XX      (SECU-) SEQUENOM INC.
XX
XX      Rosh RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI      Hoyal-Wrightson CR;
XX
XX      WPI; 2005-163257/17.
DR
XX
XX      Identifying risk of, preventing and/or treating breast cancer by
PT      identifying and/or analyzing polymorphic variations in nucleotide

```

PT sequences within the human genome.
XX
PS Example 17; Page 361; 617pp; English.
XX
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of a
CC polymorphic variation associated with breast cancer. The method of the
CC invention demonstrates cytosstatic activity and may be useful for
CC identifying a risk of, preventing and/or treating breast cancer and
CC cancer metastasis. The methods may be utilized for gene therapy or RNA
CC interference. The current sequence is that of the human mitogen-activated
CC protein kinase 10 (MAPK10) SNP-containing gDNA MAPK10-AC of the invention
CC which is located at chromosome 4q22.1-q23.
XX
SQ Sequence 823 BP; 277 A; 137 C; 113 G; 295 T; 0 U; 1 Other;
Query Match 57.9%; Score 463.4; DB 14; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.5e-95;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 336 TTGTGATGAGGCACATTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 395
DB 1 TTGTGATGAGGCACATTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 60
QY 396 TTTAAATTATTTATGAAAAAGTTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 455
DB 61 TTTAAATTATTTATGAAAAAGTTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 120
QY 456 AATGCCACACTGAATATCAAAAAGAAATPAAATCAATCAATTTAAGACACACCATGT 515
DB 121 AATGCCACACTGAATATCAAAAAGAAATPAAATCAATCAATTTAAGACACACCATGT 180
QY 516 GATATTTGTCATCTGCTCTTTAAGCAATGTATGTTATTTCTTGCAACCCCTACCAAA 575
DB 181 GATATTTGTCATCTGCTCTTTAAGCAATGTATGTTATTTCTTGCAACCCCTACCAAA 240
QY 576 GGCAGAAATTCACAGACTAGTTATGTTATTTCTTGCAACCCCTACCAAA 635
DB 241 GGCAGAAATTCACAGACTAGTTATGTTATTTCTTGCAACCCCTACCAAA 300
QY 636 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGCAATTCATTACTTCT 695
DB 301 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGCAATTCATTACTTCT 360
QY 696 TGTAGATTAAGTTCTGTAAAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 755
DB 361 TGTAGATTAAGTTCTGTAAAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 420
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATAGCTTTGATG 800
DB 421 CACAGGAAATTCATTACTTAATGCCAAATTAATAGCTTTGATG 465
RESULT 4
ADY03501.
ID ADY03501 standard; DNA; 823 BP.
AC ADY03501;
DT 05-MAY-2005 (first entry)
XX
DE Human mitogen-activated protein kinase 10 SNP-containing gDNA MAPK10-AD.
XX
XX SNP detection; breast tumor; endocrine disease;
XX gynecology and obstetrics; neoplasm; cytostatic; metastasis;
XX gene therapy; RNA interference; chromosome 4; ds; SNP;
XX single nucleotide polymorphism; mitogen-activated protein kinase 10;
XX Jun N terminal kinase-3; MAPK10.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation 539

FT
FT /tag= a
FT /standard_name= "single nucleotide polymorphism (SNP)"
XX
XX
XX WO2005014846-A2.
XX
XX 17-FEB-2005.
XX
XX 27-MAY-2004; 2004MO-US016939.
XX
XX 24-JUL-2003; 2003US-0490234P.
XX 25-NOV-2003; 2003US-00723681.
XX 25-NOV-2003; 2003US-0525239P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX Hoyal-Wrightson CR;
XX WPI; 2005-163257/17.
XX
XX
XX Identifying risk of, preventing and/or treating breast cancer by
XX identifying and/or analyzing polymorphic variations in nucleotide
XX sequences within the human genome.
XX
XX Example 17; Page 362; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer comprising detecting the presence or absence of a
XX polymorphic variation associated with breast cancer. The method of the
XX invention demonstrates cytosstatic activity and may be useful for
XX identifying a risk of, preventing and/or treating breast cancer and
XX cancer metastasis. The methods may be utilized for gene therapy or RNA
XX interference. The current sequence is that of the human mitogen-activated
XX protein kinase 10 (MAPK10) SNP-containing gDNA MAPK10-AD of the invention
XX which is located at chromosome 4q22.1-q23.
XX
SQ Sequence 823 BP; 278 A; 137 C; 112 G; 295 T; 0 U; 1 Other;
Query Match 57.9%; Score 463.4; DB 14; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.5e-95;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 336 TTGTGATGAGGCACATTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 395
DB 1 TTGTGATGAGGCACATTACCCCTTTAGCCCATGTTAACTTTCTTCAGATTCATTACTA 60
QY 396 TTTAAATTATTTATGAAAAAGTTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 455
DB 61 TTTAAATTATTTATGAAAAAGTTTTGTCTGATCATTACCATCAGAAATATCAGAAATG 120
QY 456 AATGCCACACTGAATATCAAAAAGAAATPAAATCAATCAATTTAAGACACACCATGT 515
DB 121 AATGCCACACTGAATATCAAAAAGAAATPAAATCAATCAATTTAAGACACACCATGT 180
QY 516 GATATTTGTCATCTGCTCTTTAAGCAATGTATGTTATTTCTTGCAACCCCTACCAAA 575
DB 181 GATATTTGTCATCTGCTCTTTAAGCAATGTATGTTATTTCTTGCAACCCCTACCAAA 240
QY 576 GGCAGAAATTCACAGACTAGTTATGTTATTTCTTGCAACCCCTACCAAA 635
DB 241 GGCAGAAATTCACAGACTAGTTATGTTATTTCTTGCAACCCCTACCAAA 300
QY 636 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGCAATTCATTACTTCT 695
DB 301 GAGAAAGCTGTCCTTTTACTACACCAATTTTACTCTTCTTGCAATTCATTACTTCT 360
QY 696 TGTAGATTAAGTTCTGTAAAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 755
DB 361 TGTAGATTAAGTTCTGTAAAGAAACAGCTGTGTATTTAAGAAAACAATTTATCTTCATC 420
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATAGCTTTGATG 800
DB 421 CACAGGAAATTCATTACTTAATGCCAAATTAATAGCTTTGATG 465

DE Nucleic acid sequence of JNK3 (Genbank Accn No: U34819).
XX
XX C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; disorder;
KW Alzheimer's disease; Huntington disease; amyotrophic lateral sclerosis;
KW ischemia; trauma; motor neuron disease; Parkinson's disease; epilepsy;
KW human; ss.
XX
OS Homo sapiens.
XX
PN WO9918193-A1.
XX
PD 15-APR-1999.
XX
PF 05-OCT-1998; 98WO-US020904.
XX
PR 03-OCT-1997; 97US-0060995P.
XX
XX (UYMA-) UNIV MASSACHUSETTS.
XX
PI Davis RJ, Flavell RA, Rakic P, Whitmarsh AJ, Kuan C, Yang D;
XX WPI; 1999-287734/27.
XX P-PSDB; AAY09200.
XX
PT Identification of c-Jun N-terminal kinase 3 modulators.
XX
PS Disclosure; Fig 1A; 88pp; English.
XX
XX The invention relates to a method for identifying compounds that modulate
CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method
CC comprises (a) incubating a cell that can express a JNK3 protein, or that
CC has JNK3 activity, with a compound under conditions and for a time
CC sufficient for the cell to express a JNK3 protein/activity without the
CC compound; (b) incubating a control cell under the same conditions and for
CC the same time without the compound; (c) measuring JNK3 expression/
CC activity in the cell in the presence of the compound; (d) comparing the
CC amount of JNK3 expression/activity in the presence and absence of the
CC compound, where a difference in the level of expression/activity
CC indicates that the compound modulates JNK3 expression/activity. The
CC invention also provides a transgenic non-human mammal having a transgene
CC disrupting expression of a JNK3 gene, the transgene being chromosomally
CC integrated into germ cells of the mammal. JNK3 expression inhibitor;
CC e.g. antisense nucleic acids, are used to treat disorders involving;
CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, ischemia,
CC amyotrophic lateral sclerosis, trauma, motor neuron disease, Parkinson's
CC disease or epilepsy. The present sequence represents the nucleic acid
CC sequence of human JNK3 (Genbank Accn No: U34819). JNK3 sequences under
CC Genbank accession numbers U34820, U07620, L27128, L35236, X12740 and
CC U00727 can also be used in the method of the invention. (Updated on 20-
CC MAR-2003 to correct DR field.)
XX
XX
SQ Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
XX
XX
XX Query Match 10.3%; Score 82.8; DB 2; Length 1505;
XX Best Local Similarity .97.7%; Pred. No. 6e-09;
XX Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 626 GATCCTGAAGAGAGAGCGTGTCTTTACTACACATTTTACTCTTTCTTGAATTC 685
XX |||||||
DB 1323 GCACCTGAAGAGAGAGCGTGTCTTTACTACACATTTTACTCTTTCTTGAATTC 1264
XX |||||||
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
XX |||||||
DB 1263 ATTACTCTCTGTAGATAGTTCTTT 1238
XX |||||||
XX
XX
XX RESULT 8
XX ABL88412/c
XX ID ABL88412 standard; cDNA, 1505 BP.
XX AC ABL88412;
XX KW
XX DT 16-MAY-2002 (first entry)

XX
XX Pain regulated cDNA sequence 55.
DE
XX Pain; analgesic; gene therapy; neurological disorder;
KW neurodegenerative disease; gene; ss.
XX
XX Homo sapiens.
XX
PN WO200212338-A2.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001WO-EP009011.
XX
PR 03-AUG-2000; 2000DE-01037759.
XX
XX (CHEF) GRUENTHAL GMBH.
XX
XX Gillen C, Wetzel S, Wendt S, Weihe E, Schaefer MK;
XX WPI; 2002-257469/30.
XX P-PSDB; ABB85007.
XX
XX
XX Identifying pain-regulating compounds, useful for treating chronic pain
XX and for diagnosis, by measuring binding of compounds to specific peptides
XX and proteins.
XX
XX Claim 1; Fig 34; 213pp; German.
XX
XX The invention relates to identifying pain-regulating substances (A)
CC comprises (i) incubating a test substance with a cell (or preparation
CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (ABB8411-ABL8841) that encode proteins (B, ABB85006-
CC ABB85007) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain.
CC including use in gene therapy. The same materials can also be used for
CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC present sequence is that of a polynucleotide of the invention
XX
XX
SQ Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
XX
XX
XX Query Match 10.3%; Score 82.8; DB 6; Length 1505;
XX Best Local Similarity .97.7%; Pred. No. 6e-09;
XX Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 626 GATCCTGAAGAGAGAGCGTGTCTTTACTACACATTTTACTCTTTCTTGAATTC 685
XX |||||||
DB 1323 GCACCTGAAGAGAGAGCGTGTCTTTACTACACATTTTACTCTTTCTTGAATTC 1264
XX |||||||
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
XX |||||||
DB 1263 ATTACTCTCTGTAGATAGTTCTTT 1238
XX |||||||
XX
XX
XX RESULT 9
XX AD131626/c
XX ID AD131626 standard; cDNA, 1505 BP.
XX AC AD131626;
XX XX
XX 17-JUN-2004 (first entry)
XX
XX Human cDNA #952.
XX
XX Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypersplenophilia;
KW irritative bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antisthmatic; antiulcer;
KW osteopathic; anticholinergic; antineumatic; cytostatic.

```
XX OS Homo sapiens.
XX PN US6607879-B1.
XX PD 19-AUG-2003.
XX PF 09-FEB-1998; 98US-00023655.
XX PR 09-FEB-1998; 98US-00023655.
XX PA (INCYTE CORP.
XX PI Cocke BG, Stuart SG, Seilhamer JJ;
XX DR WPI; 2003-895307/82.
XX PT A composition comprising a plurality of cDNAs, useful for detecting
XX PT altered expression of genes in an immunological response or for
XX PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX PT or osteoarthritis.
XX PS Claim 1; SEQ ID NO 952; 50pp; English.
XX CC The invention relates to a composition comprising a plurality of cDNAs
XX CC for detecting the altered expression of genes in an immunological
XX CC response. The invention also relates to a method of diagnosing or
XX CC monitoring the treatment of an immunopathological condition in a sample,
XX CC comprising obtaining nucleic acids from a sample, contacting the nucleic
XX CC acids of the sample with an array comprising the plurality of cDNAs under
XX CC conditions to form one or more hybridisation complexes, detecting the
XX CC hybridisation complexes and comparing the levels of the detected
XX CC hybridisation complexes with the level of hybridisation complexes
XX CC detected in a non-diseased sample, where an altered level of the detected
XX CC hybridisation complexes correlates with the presence of an
XX CC immunopathological condition. Also disclosed are an expression profile
XX CC comprising a microarray and a plurality of detectable complexes and a
XX CC method for identifying a plurality of polynucleotide probes. The cDNAs
XX CC are useful as hybridisable array elements in a microarray for monitoring
XX CC the expression of target polynucleotides. The microarray can be used in
XX CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX CC ulcerative colitis, hyper eosinophilia, irritable bowel syndrome,
XX CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX CC identifying agents for the treatment of the diseases. The microarray may
XX CC also be used in drug discovery and development, toxicological and
XX CC carcinogenicity studies, forensics or pharmacogenomics. The composition
XX CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
XX CC genomic fragments. This sequence represents a human cDNA of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification but was obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
XX
XX Query Match 10.3%; Score 82.8; DB 11; Length 1505;
XX Best Local Similarity 97.7%; Pred. No. 6e-09;
XX Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 626 GTACCTGAAGAGAGAGGCTGTCCTTTACTACACATTTTGTAGTCTTTCTGTAATC 685
XX DB 1323 GCACCTGAAGAGAGAGGCTGTCCTTTACTACACATTTTGTAGTCTTTCTGTAATC 1264
XX
XX QY 686 ATTACTCTCTGTAGATAAGTTCTGT 711
XX DB 1263 ATTACTCTCTGTAGATAAGTTCTTT 1238
XX
XX RESULT 10
XX ADS83693/c
XX ID ADS83693 standard; cDNA; 1505 BP.
XX AC ADS83693;
XX XX
```

```
DT 11-AUG-2005 (first entry)
XX DE Human lymph node cDNA #952.
XX KW ss; gene; human; immunological response; blood cell; cancer;
XX KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
XX KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
XX KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX OS Homo sapiens.
XX PN US2004077003-A1.
XX PD 22-APR-2004.
XX PF 14-AUG-2003; 2003US-00641643.
XX PR 09-FEB-1998; 98US-00023655.
XX PA (INCYTE CORP.
XX PI Cocke BG, Stuart SG, Seilhamer JJ;
XX DR WPI; 2004-387937/36.
XX PT New compositions having a number of first, second and third
XX PT polynucleotide probes, useful in research and diagnostic applications in
XX PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
XX PT infections.
XX PS Claim 15; SEQ ID NO 952; 16pp; English.
XX CC The invention relates to polynucleotides which are used as probes to
XX CC detect genes differentially expressed in an immunological response,
XX CC abundantly expressed in an immunological response and/or coding for a
XX CC polypeptide known to regulate blood cell biology. The polynucleotides are
XX CC useful in research and diagnostic applications particularly in cancer and
XX CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
XX CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
XX CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
XX CC present sequence represents a human lymph node cDNA used to detect blood
XX CC cell and immunological response gene expression. Note: The present
XX CC sequence does not appear in the printed specification but was obtained in
XX CC electronic format from the USPTO web site
XX CC (seqdata.uspto.gov/sequence.html?docid=20040077003).
XX SQ Sequence 1505 BP; 459 A; 343 C; 346 G; 357 T; 0 U; 0 Other;
XX
XX Query Match 10.3%; Score 82.8; DB 13; Length 1505;
XX Best Local Similarity 97.7%; Pred. No. 6e-09;
XX Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 626 GTACCTGAAGAGAGAGGCTGTCCTTTACTACACATTTTGTAGTCTTTCTGTAATC 685
XX DB 1323 GCACCTGAAGAGAGAGGCTGTCCTTTACTACACATTTTGTAGTCTTTCTGTAATC 1264
XX
XX QY 686 ATTACTCTCTGTAGATAAGTTCTGT 711
XX DB 1263 ATTACTCTCTGTAGATAAGTTCTTT 1238
XX
XX RESULT 11
XX AEG09274/c
XX ID AEG09274 standard; DNA; 2211 BP.
XX AC AEG09274;
XX XX
XX DT 20-APR-2006 (first entry)
XX DE Human MAPK10, transcript variant 2 DNA.
XX KW amyloid-beta precursor protein; pharmaceutical;
XX KW mitogen activated protein-kinase inhibitor; neurological disease;
XX KW
```

	XX	Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
KW	MOORECROPIC; substrate; mitogen-activated protein kinase 10; MAPK10; Ras gene.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	
FT	CDS	
FT	Location/Qualifiers	
FT	68..1462	
FT	/tag=a	
FT	/product="mitogen-activated protein kinase 10 (MAPK10), transcript variant 2"	
XX		
PN	WO2005109001-A2.	
PD		
PD	17-NOV-2005.	
XX		
PF	12-MAY-2005; 2005WO-EP052182.	
XX		
PR	12-MAY-2004; 2004US-0570352P.	
PR	24-AUG-2004; 2004US-0603948P.	
PA	(GALA-) GALAPAGOS GENOMICS NV.	
EA	(LAEN/) LAENEN W.	
PI	Spititaele KF, Hoffmann M, Merchiers PG;	
XX		
PI	WPI; 2006-231019/24.	
DR	P-Psdb; AEG09283.	
DR	REFSEQ; NM_138982.	
XX		
PT	Identifying a compound that inhibits amyloid-beta precursor protein processing in a mammalian cell for treating e.g., Alzheimer's disease by measuring a compound-polypeptide property related to amyloid-beta peptide production.	
XX		
PS	Example 1; SEQ ID NO 10; 84pp; English.	
XX		
CC	This invention describes a novel method of identifying a compound that inhibits the processing of amyloid-beta precursor protein in a mammalian cell. The invention also describes; a) an agent for inhibiting amyloid-beta precursor processing consisting of an antisense polynucleotide; a ribozyme or a small interfering RNA (siRNA), where the agent comprises a nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence encoding the polypeptide comprising the amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical; composition comprising the agent for inhibiting amyloid-beta precursor processing or an amyloid-beta precursor processing-inhibiting amount of a mitogen activated protein-kinase inhibitor in admixture with a carrier. The method involves activation of a biological pathway producing an indicator of the processing of amyloid-beta precursor protein e.g. a phosphorylated substrate of a kinase comprising AEG09286-AEG09268. The indicator induces the expression of a reporter e.g. alkaline phosphatase, GFP, egFP, dGFP, luciferase or beta-galactosidase in the mammalian cell. The pharmaceutical composition further comprises a label indicating use of the composition for treating or preventing a condition involving cognitive impairment or a susceptibility to the condition. The agent is useful in the manufacture of a medicament for inhibiting the processing of amyloid-beta precursor protein in a subject suffering from or susceptible to the abnormal processing of the protein, or for treating or preventing a condition involving cognitive impairment or a susceptibility to the condition, preferably, Alzheimer's disease. This sequence encodes human mitogen-activated protein kinase 10 (MAPK10), transcript variant 2, a kinase involved in the up-regulation of amyloid-beta 1-42.	
XX		
XX	Sequence 2211 BP; 674 A; 498 C; 482 G; 557 T; 0 U; 0 Other;	
QY	Query Match 10.3%; Score 82.8; DB 15; Length 2211;	
Bd	Best Local Similarity 97.7%; Pred. No. 6.5e-09;	
	Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
	626 GTACTGAAGAAGAAAGCTGTCTTTTACTACCACTTTTATGCTTTCTTGAAATTC 685	
	1323 GCACCTGAAGGAAGGGCTGTCTTTTACTACCACTTTTATGCTTTCTTGAAATTC 1266	

QY 686 ATTACTTCCTGTGATGATGATCTTGT 711
 |||
 DB 1263 ATTACTTCCTGTGATGATGATCTT 1238

 RESULT 12
 AAX37267/C
 ID AAX37267 standard; DNA: 2367 BP.
 XX
 AC AAX37267;
 XX
 DT 20-MAR-2003 (revised)
 DT 21-JUL-1999 (first entry)
 XX
 DE Seq ID No: 3 of W09918193.
 XX
 KW C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; disorder;
 KW Alzheimer's disease; Huntington disease; amyotrophic lateral sclerosis;
 KW ischemia; trauma; motorneuron disease; Parkinson's disease; epilepsy;
 KW human; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09918193-A1.
 XX
 PD 15-APR-1999.
 XX
 PF 05-OCT-1998; 98WO-US020904.
 XX
 PR 03-OCT-1997; 97US-0060995P.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Davis RJ, Flavell RA, Rakic P, Whitmarsh AJ, Kuan C, Yang D;
 DR WPI: 1999-287734/27.
 XX
 PT Identification of c-Jun N-terminal kinase 3 modulators.
 XX
 PS Disclosure; Fig 1C; 88pp; English.
 XX
 CC The invention relates to a method for identifying compounds that modulate
 CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method
 CC comprises (a) incubating a cell that can express a JNK3 protein, or that
 CC has JNK3 activity, with a compound under conditions and for a time
 CC sufficient for the cell to express a JNK3 protein/activity without the
 CC compound; (b) incubating a control cell under the same conditions and for
 CC the same time without the compound; (c) measuring JNK3 expression/
 CC activity in the cell in the presence of the compound; (d) comparing the
 CC amount of JNK3 expression/activity in the presence and absence of the
 CC compound, where a difference in the level of expression/activity
 CC indicates that the compound modulates JNK3 expression/activity. The
 CC invention also provides a transgenic non-human mammal having a transgene
 CC disrupting expression of a JNK3 gene, the transgene being chromosomally
 CC integrated into germ cells of the mammal. JNK3 expression inhibitors,
 CC e.g. antisense nucleic acids, are used to treat disorders involving
 CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, ischemia,
 CC amyotrophic lateral sclerosis, trauma, motorneuron disease, Parkinson's
 CC disease or epilepsy. JNK3 sequences under Genbank accession numbers
 CC U34819, U34820, U07620, U27128, U35236, X12740 and V00727 can be used in
 CC the method of the invention. (Updated on 20-MAR-2003 to correct DR
 CC field.)
 CC
 XX
 SQ Sequence 2367 BP; 712 A; 546 C; 518 G; 591 T; 0 U; 0 Other;
 Query Match 10.3%; Score 82.8; DB 2; Length 2367;
 Best Local Similarity 97.7%; Pred. No. 6,6e-09;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 626 GTACTCTGAAGAGAGGCTGTCTTTTACTACACACATTTTACTCTTCTTCGATTC 685
 DB 1479 GCACCTTAAGAGAGAGGCTGTCTTTTACTACACACATTTTACTCTTCTTCGAAATTC 1420

OY 686 ATTACTCTCTGTGATAGTTCNGT 711
 DB 1419 ATTACTCTCTGTGATAGTTCCTT 1394

RESULT 13
 ADI61666/c
 ID ADI61666 standard; cDNA; 2677 BP.

AC ADI61666;

DT 22-APR-2004 (first entry)

DE Human cDNA downregulated in Alzheimer's disease, INCYTE 413797.5.

KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
 brain disorder.

OS Homo sapiens.

PN US668288-B1.

PD 27-JAN-2004.

PF 05-MAY-2000; 2000US-00566921.

PR 05-MAY-2000; 2000US-00566921.

PA (INCY-) INCYTE CORP.

PI Loring JF, Tingley DW, Edwards CM;

DR WPI; 2004-118572/12.

PT New composition comprising cDNAs that are differentially expressed in
 brain disorders, useful for diagnosing or treating Alzheimer's disease.

PS Claim 1; SEQ ID NO 34; 223pp; English.

XX The invention relates to a new composition comprising ADI61633-
 CC ADI6170 and their complements that are cDNAs differentially expressed in
 CC brain disorders. Also included are a high throughput method for detecting
 CC differential expression of one or more cDNAs in a sample containing
 CC nucleic acids and a high throughput method for screening a library of
 CC molecules or compounds to identify a ligand that specifically binds a
 CC cDNA. The expression of the each of the cDNAs is downregulated at least
 CC two-fold in the brain of the subjects with Alzheimer's disease (ADI61727)
 CC ADI61727) or upregulated at least two fold in Alzheimer's disease
 CC (ADI61728-ADI61770). The composition is useful for diagnosing or treating
 CC Alzheimer's disease. The present sequence is a cDNA downregulated at
 CC least two-fold in the brain of the subjects with Alzheimer's disease.
 CC
 SQ Sequence 2677 BP; 785 A; 598 C; 581 G; 712 T; 0 U; 1 Other;

Query Match 10.3%; Score 82.8; DB 12; Length 2677;
 Best Local Similarity 97.7%; Pred. No. 6.8e-09;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 626 GTACCGAAGAGAGAGGCTCTCTTTACTACACCAATTTTACTCTTTCTTGAATTC 685
 DB 1795 GACACGAGAGAGAGAGGCTCTCTTTACTACACCAATTTTACTCTTTCTTGAATTC 1736
 OY 686 ATTACTCTCTGTGATAGTTCGT 711
 DB 1735 ATTACTCTCTGTGATAGTTCCTT 1710

RESULT 14
 AEA43831/c
 ID AEA43831 standard; cDNA; 2677 BP.
 AC AEA43831;

XX 25-AUG-2005 (first entry)
 DT
 DE Human cDNA differentially expressed in brain tissue SEQ ID NO:34.

XX diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
 KM muscular-gen.; cytosolic; neuroleptic; nootropic; antidepressant;
 KM anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
 KM immunotherapy; gene therapy; ss.

OS Homo sapiens.

PN US2005130171-A1.

PD 16-JUN-2005.

PF 26-JAN-2004; 2004US-00765700.

PR 05-MAY-2000; 2000US-00566921.

PA (INCY-) INCYTE CORP.

PI Loring JF, Tingley DW, Edwards CM;

DR WPI; 2005-456990/46.

PT Composition useful for diagnosis, staging, treating or monitoring
 treatment of a subject with a brain disorder, comprising several cDNAs
 that are differentially expressed in brain disorders.

PS Claim 1; SEQ ID NO 34; 231pp; English.

XX The invention relates to a composition (I) for the diagnosis, staging,
 CC treatment or for the monitoring of treatment of a subject with a brain
 CC disorder. (I) comprises several cDNAs that are differentially expressed
 CC in brain disorders and chosen from any one of 138 nucleotide sequences of
 CC AEA43798-AEA43935, or their complements. Also described: (1) a high
 CC throughput method for detecting differential expression of one or more
 CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II)
 CC selected from AEA43812, AEA43813, AEA43830, AEA43831, AEA43855, AEA43856,
 CC AEA43883 and AEA43923; (3) an expression vector (III) containing (II);
 CC (4) a host cell (IV) containing (III); (5) a protein (V) produced using
 CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful
 CC for a high throughput method of screening a library of molecules or
 CC compounds to identify a ligand which specifically binds a cDNA, where the
 CC method involves combining (I) with the library of molecules or compound
 CC under conditions to allow specific binding and detecting specific binding
 CC between each cDNA and a molecule or compound. (IV) is useful for
 CC producing a protein, which involves culturing (IV) under conditions for
 CC the expression of the protein and recovering the protein from the
 CC culture. (V) is useful for high throughput method for screening a library
 CC of molecules or compounds to identify a ligand which specifically binds
 CC (V), where the method involves combining (V) or its portion with the
 CC library of molecules or compound under conditions to allow specific
 CC binding and detecting specific binding between (V) and a molecule or
 CC compound. (V) is useful for purifying a ligand from a sample, which
 CC involves combining (V) or its portion with the sample under conditions to
 CC allow specific binding, recovering the bound protein and separating the
 CC protein from ligand. (V) is also useful for producing an antibody, which
 CC involves immunizing an animal with (V) or its portion under conditions to
 CC elicit an antibody response, isolating animal antibodies and screening
 CC the isolated antibodies with the protein. (II) is useful in gene therapy
 CC for the treatment or prevention of conditions and disorders associated
 CC with immune response. The present sequence represents a human cDNA
 CC sequence which is differentially expressed in brain tissues, which is
 CC used in the exemplification of the present invention.
 CC
 SQ Sequence 2677 BP; 785 A; 598 C; 581 G; 712 T; 0 U; 1 Other;

Query Match 10.3%; Score 82.8; DB 14; Length 2677;

Best Local Similarity 97.7%; Pred. No. 6.8e-09;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	620	GPACCTGAAGAGAAAGCGTCTCTTACTACACATTTAGTCCTTTCTCGAATC	669
Db	1795	GCACCTGAAGAGAAAGCGTCTCTTACTACACATTTAGTCCTTTCTCGAATC	1733
Qy	686	ATTACTTCTCTGTAGATTAAGTTCTGT	711
Db	1735	ATTACTTCTCTGTAGATTAAGTTCTTT	1710
RESULT 15			
AEG09275/c			
AEG09275	standard; DNA; 2698 BP.		
AC	AEG09275;		
XX			
XX			
DT	20-APR-2006	(first entry)	
XX			
DE	Human MAPK10, transcript variant 3 DNA.		
XX			
KM	amyloid-beta precursor protein; pharmaceutical;		
KM	mitogen activated protein-kinase inhibitor; neurological disease;		
KM	Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;		
KM	Neurotropic; substrate; mitogen-activated protein Kinase 10; MAPK10; de		
KM	gene.		
XX			
OS	Homo sapiens.		
XX			
XX			
FT	Key	Location/Qualifiers	
FT	CDS	669..1949	
FT		/tag= a	
FT		/product= "mitogen-activated protein kinase 10 (MAPK10),	
FT		transcript variant 3"	
PN	W02005109001-A2.		
PD			
XX	17-NOV-2005.		
XX			
PP	12-MAY-2005; 2005WO-EP052182.		
PR	12-MAY-2004; 2004US-0570352P.		
PR	24-AUG-2004; 2004US-0603948P.		
PA	(GALA-) GALAPAGOS GENOMICS NV.		
PA	(LAEN) LAENEN W.		
XX			
PI	Spitzels KE, Hoffmann M, Merchiers PG;		
XX			
DR	WPI; 2006-231019/24.		
DR	P-PSDB; AEG09284.		
DR	REFSEQ; NM_138980.		
XX			
PT	Identifying a compound that inhibits amyloid-beta precursor protein		
PT	processing in a mammalian cell for treating e.g., Alzheimer's disease by		
PT	measuring a compound-polypeptide property related to amyloid-beta peptide		
PT	production.		
XX			
PS	Example 1; SEQ ID NO 11; 84bp; English.		
XX			
CC	This invention describes a novel method of identifying a compound that		
CC	inhibits the processing of amyloid-beta precursor protein in a mammalian		
CC	cell. The invention also describes; a) an agent for inhibiting amyloid-		
CC	beta precursor processing consisting of an antisense polynucleotide; a		
CC	ribozyme or a small interfering RNA (siRNA), where the agent comprises a		
CC	nucleic acid sequence complementary to, or engineered from, a naturally-		
CC	occurring polynucleotide sequence encoding the polypeptide comprising the		
CC	amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical		
CC	composition comprising the agent for inhibiting amyloid-beta precursor		
CC	processing or an amyloid-beta precursor processing-inhibiting amount of a		
CC	mitogen activated protein-kinase inhibitor in admixture with a carrier.		
CC	The method involves activation of a biological pathway producing an		
CC	indicator of the processing of amyloid-beta precursor protein e.g. a		
CC	phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The		
CC	indicator induces the expression of a reporter e.g. alkaline phosphatase,		
CC			

Query Match	Best Local Similarity	Score	DB 15;	Length	2698;
Matches	84;	Conservative	0;	Mismatches	2;
				Indels	0;
				Gaps	0
626 GTACCTGAGAGAGAGGCTGCTCTTTACTACACCATTTTAACTCTTCTTCTGAATTC	1810 GCACCTGAGAGAGAGGCTGCTCTTTACTACACCATTTTAACTCTTCTTCTGAATTC	175			
686 ATTACTTCTCTTGTGATTAAGTTCTTCTGT	1750 ATTACTTCTCTTGTGATTAAGTTCTTCTGT	1725			
RESULT 16					
AAS93582/c					
AAS93582 standard; cDNA; 972 BP.					
AAS93582;					
13-FEB-2002 (first entry)					
DNA encoding novel human diagnostic protein #29386.					
Human; chromosome mapping; gene mapping; gene therapy; forensic;					
Food supplement; medical imaging; diagnostic; genetic disorder; ss.					
Homo sapiens.					
WO200175067-A2.					
11-OCT-2001.					
30-MAR-2001; 2001WO-US008631.					
31-MAR-2000; 2000US-00540217.					
23-AUG-2000; 2000US-00649167.					
(HYSE-) HYSEQ INC.					
Dmanac RT, Liu C, Tang YT;					
WPI: 2001-639362/73.					
P-PSDB; ABG29395.					
New isolated polynucleotide and encoded polypeptides, useful in					
diagnostics, forensics, gene mapping, identification of mutations					
responsible for genetic disorders or other traits and to assess					
biodiversity.					
Claim 1; SEQ ID NO 29386; 103bp; English.					
The invention relates to isolated polynucleotide (I) and polypeptide (II)					
sequences. (I) is useful as hybridisation probes, polymerase chain					
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,					
and in recombinant production of (II). The polynucleotides are also used					
in diagnostics as expressed sequence tags for identifying expressed					
genes. (I) is useful in gene therapy techniques to restore normal					
activity of (II) or to treat disease states involving (II). (II) is					
useful for generating antibodies against it, detecting or quantitating a					

CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 972 BP; 202 A; 268 C; 312 G; 190 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 5; Length 972;
Best Local Similarity 98.8%; Pred. No. 1.9e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAATTCAT 687
DB 453 AGCTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAATTCAT 394
QY 688 TACTTCCTTGTAGATAGTTCT 709
DB 393 TACTTCCTTGTAGATAGTTCT 372

RESULT 17
AAS66964/c
ID AAS66964 standard; cDNA; 999 BP.
AC AAS66964;
XX
XX
XX 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #2768.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR P-PSDB; ABG02777.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnosis, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX
XX Claim 1; SEQ ID NO 2768; 103bp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 999 BP; 221 A; 277 C; 313 G; 188 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 5; Length 999;
Best Local Similarity 98.8%; Pred. No. 1.9e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAATTCAT 687
DB 453 AGCTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAATTCAT 394
QY 688 TACTTCCTTGTAGATAGTTCT 709
DB 393 TACTTCCTTGTAGATAGTTCT 372

RESULT 18
AAS75684/c
ID AAS75684 standard; cDNA; 1111 BP.
AC AAS75684;
XX
XX
XX 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #11488.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR P-PSDB; ABG11497.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnosis, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX
XX Claim 1; SEQ ID NO 11488; 103bp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used

CC from (t) that has synthesized a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (AB88411-AB88441) that encode proteins (B, AB885006-
CC AB885037) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain,
CC including use in gene therapy. The same materials can also be used for
CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC present sequence is that of a polynucleotide of the invention
XX

Seq Sequence 1773 BP; 555 A; 410 C; 388 G; 420 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 6; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCTGCTCTTTACTACACCATTTTATGCTTTCTTCTGAATTCATTA 689
DB 1343 CTGAAGAGAGAGAGCTGCTCTTTACTACACCATTTTATGCTTTCTTCTGAATTCATTA 1284

QY 690 CTTCTCTTGATGATTAAGTTCTGT 711
DB 1283 CTTCTCTTGATGATTAAGTTCTTT 1262

RESULT 21
AED32365/c
ID AED32365 standard; DNA; 1773 BP.
XX
AC AED32365;
XX
DT 15-DEC-2005 (first entry)
XX
DE Human promyelocytic leukemia protein kinase encoding gene, SEQ ID 7.
XX
KM differentiation; cytostatic; acute promyelocytic leukemia; gene; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 92..1360
FT /*tag= a
FT /product= "Human promyelocytic leukemia protein kinase"
XX
PN JP2005281183-A.
XX
PD 13-OCT-2005.
XX
PF 29-MAR-2004; 2004JP-00097088.
XX
PR 29-MAR-2004; 2004JP-00097088.
XX
PA (KOKU-) KOKURITSU GAN CENT SOCHO.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.
XX
PI Kitabayashi K;
XX
XX WPI; 2005-717904/74.
DR P-PSDB; AED32366.
XX
PT Differentiation inducing agent of leukemia cell useful as leukemia
PT therapeutic agent, comprises expression activator/functional activator of
PT promyelocytic leukemia protein, or expression inhibitor/functional
PT inhibitor of PMLK protein.
XX
PS Disclosure; SEQ ID NO 7; 28pp; Japanese.
XX
CC The invention relates to a novel differentiation inducing agent of a
CC leukemia cell. The agent comprises an expression activator or functional
CC activator of a promyelocytic leukemia (PML) protein, or an expression
CC inhibitor or functional inhibitor of the PMLK protein (a PML specific

CC protein phosphorylation enzyme). The invention further comprises a
CC screening method for the promyelocytic leukemia protein. The
CC differentiation inducing agent is useful as a therapeutic agent of
CC leukemia. This polynucleotide sequence represents the gene encoding a
CC human promyelocytic leukemia protein kinase (PMLK) of the invention.
XX

Seq Sequence 1773 BP; 555 A; 410 C; 388 G; 420 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 14; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCTGCTCTTTACTACACCATTTTATGCTTTCTTCTGAATTCATTA 689
DB 1343 CTGAAGAGAGAGAGCTGCTCTTTACTACACCATTTTATGCTTTCTTCTGAATTCATTA 1284

QY 690 CTTCTCTTGATGATTAAGTTCTGT 711
DB 1283 CTTCTCTTGATGATTAAGTTCTTT 1262

RESULT 22
AAS83445/c
ID AAS83445 standard; cDNA; 1872 BP.
XX
AC AAS83445;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19249.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
PI WPI; 2001-639362/73.
DR P-PSDB; AEG19258.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
PS Claim 1; SEQ ID NO 19249; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1872 BP; 459 A; 499 C; 520 G; 394 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 5; Length 1872;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 628 ACCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCAT 687
DB 453 AGCTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCAT 394
QY 688 TACTTCTCTGTAGTAAGTTCT 709
DB 393 TACTTCTCTGTAGTAAGTTCT 372
RESULT 23
ID AEG09276/c standard; DNA; 2155 BP.
XX
AC AEG09276;
XX
DT 20-APR-2006 (first entry)
XX
DE Human MAPK10, transcript variant 4 DNA.
XX
KM amyloid-beta precursor protein; pharmaceutical;
KM mitogen activated protein-kinase inhibitor; neurological disease;
KM Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
KM Neurotropic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
KM gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 442..1275
FT /tag= a
FT /product= "mitogen-activated protein kinase 10 (MAPK10),
FT transcript variant 4"
XX
PN MO2005109001-A2.
XX
PD 17-NOV-2005.
XX
PF 12-MAY-2005; 2005MO-EP052182.
XX
PR 12-MAY-2004; 2004US-0570352P.
PR 24-AUG-2004; 2004US-0603948P.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
XX
PA (LAEN/) LAENEN W.
XX
PI Splitteale KF, Hoffmann W, Merchiers PG;
XX
DR WPI; 2006-231019/24.
DR P-PDB; AEG09285.
DR REFSO; NM_138981.
XX
XX Identifying a compound that inhibits amyloid-beta precursor protein
PT processing in a mammalian cell for treating e.g., Alzheimer's disease by
PT measuring a compound-polypeptide property related to amyloid-beta peptide
PT production.
XX
PS Example 1; SEQ ID NO 12; 84bp; English.
XX
CC This invention describes a novel method of identifying a compound that

CC inhibits the processing of amyloid-beta precursor protein in a mammalian
CC cell. The invention also describes; a) an agent for inhibiting amyloid-
CC beta precursor processing consisting of an antisense polynucleotide, a
CC ribozyme or a small interfering RNA (siRNA), where the agent comprises a
CC nucleic acid sequence complementary to, or engineered from, a naturally-
CC occurring polynucleotide sequence encoding the polypeptide comprising the
CC amino acid sequence of AEG09276 or AEG09279 and b) a pharmaceutical
CC composition comprising the agent for inhibiting amyloid-beta precursor
CC processing or an amyloid-beta precursor processing-inhibiting amount of a
CC mitogen activated protein-kinase inhibitor in admixture with a carrier.
CC The method involves activation of a biological pathway producing an
CC indicator of the processing of amyloid-beta precursor protein e.g. a
CC phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The
CC indicator induces the expression of a reporter e.g. alkaline phosphatase,
CC GFP, egFP, dGFP, luciferase or beta-galactosidase in the mammalian cell.
CC The pharmaceutical composition further comprises a label indicating use
CC of the composition for treating or preventing a condition involving
CC cognitive impairment or a susceptibility to the condition. The agent is
CC useful in the manufacture of a medicament for inhibiting the processing
CC of amyloid-beta precursor protein in a subject suffering from or
CC susceptible to the abnormal processing of the protein, or for treating or
CC preventing a condition involving cognitive impairment or a susceptibility
CC to the condition, preferably, Alzheimer's disease. This sequence encodes
CC human mitogen-activated protein kinase 10 (MAPK10), transcript variant 4,
CC a kinase involved in the up-regulation of amyloid-beta 1-42.
XX
SQ Sequence 2155 BP; 629 A; 508 C; 446 G; 572 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 15; Length 2155;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCATTA 689
DB 1258 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTGTCTTTCTTGAAATTCATTA 1199
QY 690 CTTCCTGTAGTAAGTTCTGT 711
DB 1198 CTTCCTGTAGTAAGTTCTTT 1177
RESULT 24
ID AAX37276/c standard; DNA; 2372 BP.
XX
AC AAX37276;
XX
DT 20-MAR-2003 (revised)
DT 21-JUL-1999 (first entry)
XX
XX Seq ID No: 6 of WO9918193.
XX
DE C-Jun N-terminal kinase 3; JNK3; transgene; excitotoxicity; disorder;
XX
KM Alzheimer's disease; Huntington disease; amyotrophic lateral sclerosis;
KM ischemia; trauma; motorneuron disease; Parkinson's disease; epilepsy;
KM human; ss.
XX
XX Homo sapiens.
XX
OS Homo sapiens.
XX
PN WO9918193-A1.
XX
PD 15-APR-1999.
XX
PF 05-OCT-1998; 98MO-US020904.
XX
PR 03-OCT-1997; 97US-0060995P.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
PI Davis RJ, Flavell RA, Rakic P, Whitmarsh AJ, Kuan C, Yang D;
XX
DR WPI; 1999-287734/27.
XX

PT Identification of c-Jun N-terminal kinase 3 modulators.
 XX
 PS Disclosure; Fig 2D; 88pp; English.
 XX
 CC The invention relates to a method for identifying compounds that modulate
 CC c-Jun N-terminal kinase 3 (JNK3) expression or activity. The method
 CC comprises (a) incubating a cell that can express a JNK3 protein, or that
 CC has JNK3 activity, with a compound under conditions and for a time
 CC sufficient for the cell to express a JNK3 protein/activity without the
 CC compound; (b) incubating a control cell under the same conditions and for
 CC the same time without the compound; (c) measuring JNK3 expression and
 CC activity in the cell in the presence of the compound; (d) comparing the
 CC amount of JNK3 expression/activity in the presence and absence of the
 CC compound, where a difference in the level of expression/activity
 CC indicates that the compound modulates JNK3 expression/activity. The
 CC invention also provides a transgenic non-human mammal having a transgene
 CC disrupting expression of a JNK3 gene, the transgene being chromosomally
 CC integrated into germ cells of the mammal. JNK3 expression inhibitors,
 CC e.g. antisense nucleic acids, are used to treat disorders involving
 CC excitotoxicity, e.g. Alzheimer's disease, Huntington disease, ischemia,
 CC amyotrophic lateral sclerosis, trauma, motor neuron disease, Parkinson's
 CC disease or epilepsy. JNK3 sequences under Genbank accession numbers
 CC U34819, U34820, U07620, L27128, U35235, X12740 and V00727 can be used in
 CC the method of the invention. (Updated on 20-MAR-2003 to correct DR
 CC field.)
 CC
 XX
 SO Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0 U; 0 Other;
 Query Match 10.1%; Score 80.4; DB 2; Length 2372;
 Best Local Similarity 98.8%; Pred. No. 2.3e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 YY 630 CTGAAGAGAGAGCGTCTCTTCTTCTACACATTTTACGTTCTTCTTGAATTCATTA 689
 DB 1475 CTGAAGAGAGAGCGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTGAATTCATTA 1416
 YY 690 CTTCTCTGTAGATTAAGTTCTGT 711
 DB 1415 CTTCTCTGTAGATTAAGTTCTTT 1394
 RESULT 25
 AAL48611/c
 XX AAL48611 standard; cDNA; 2372 BP.
 AC AAL48611;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Human insulin receptor signaling modifier cDNA SEQ ID NO: 5.
 XX
 KW Human; insulin receptor signaling; insulin receptor signaling modifier;
 KW ISM; diabetes; metabolic syndrome; antidiabetic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200255664-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 11-JAN-2002; 2002MO-US001048.
 XX
 PR 12-JAN-2001; 2001US-0261226P.
 PR 12-JAN-2001; 2001US-0261303P.
 PR 12-JAN-2001; 2001US-0261304P.
 PR 12-JAN-2001; 2001US-0261335P.
 PR 12-JAN-2001; 2001US-0261336P.
 PR 12-JAN-2001; 2001US-0261361P.
 PR 12-JAN-2001; 2001US-0261456P.
 PR 12-JAN-2001; 2001US-0261457P.
 PR 12-JAN-2001; 2001US-0261458P.
 PR 12-JAN-2001; 2001US-0261459P.
 PR 12-JAN-2001; 2001US-0261461P.

PR 12-JAN-2001; 2001US-0261518P.
 PR 12-JAN-2001; 2001US-0261531P.
 PR 12-JAN-2001; 2001US-0261532P.
 PR 12-JAN-2001; 2001US-0261589P.
 PR 12-JAN-2001; 2001US-0261590P.
 PR 12-JAN-2001; 2001US-0261649P.
 PR 12-JAN-2001; 2001US-0261694P.
 PR 12-JAN-2001; 2001US-0261695P.
 PR 12-JAN-2001; 2001US-0261697P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Seidel-Dugan C, Ferguson KC, Kidd T;
 XX
 DR WPI; 2002-559664/64.
 DR P-PSDB; AAO18492.
 XX
 PT Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent.
 XX
 PS Disclosure; Page 39-41; 232pp; English.
 XX
 CC The present invention relates to a method of identifying a candidate
 CC insulin receptor (INR) signaling modulating agent, involving contacting
 CC an assay system comprising an insulin receptor signaling modifier (ISM)
 CC polypeptide or nucleic acid with a test agent, and detecting a test agent
 CC biased activity of the assay system. The method is useful for
 CC identifying candidate INR signaling modulating agents. ISM genes may be
 CC used as drug targets for treatment of disorders related to INR signaling
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and
 CC polypeptides are useful for identifying and testing agents that modulate
 CC ISM function and for other applications related to the involvement of ISM
 CC in INR signaling, and for identifying subjects having a predisposition to
 CC such diseases associated with INR signaling. The present sequence is an
 CC ISM coding sequence described in the exemplification of the invention
 XX
 SO Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0 U; 0 Other;
 Query Match 10.1%; Score 80.4; DB 6; Length 2372;
 Best Local Similarity 98.8%; Pred. No. 2.3e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 YY 630 CTGAAGAGAGAGCGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTGAATTCATTA 689
 DB 1475 CTGAAGAGAGAGCGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTGAATTCATTA 1416
 YY 690 CTTCTCTGTAGATTAAGTTCTGT 711
 DB 1415 CTTCTCTGTAGATTAAGTTCTTT 1394
 RESULT 26
 ACAS6791/c
 XX ACAS6791 standard; cDNA; 2372 BP.
 AC ACAS6791;
 XX
 DT 06-JUN-2003 (first entry)
 XX
 DE Human signaling pathway polynucleotide probe SEQ ID NO 1389.
 XX
 KW Human; probe; ss; array element; Parkinson's disease;
 KW signaling pathway population; cancer; adenocarcinoma; leukaemia;
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 XX
 OS Homo sapiens.
 XX
 PN US6500938-B1.
 XX
 PD 31-DEC-2002.
 XX
 PF 30-JAN-1998; 98US-00016434.

```
XX 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Sellhammer JU;
XX WPI, 2003-352189/33.
XX
XX Combination of polynucleotide probes, useful as array elements in a
XX microarray for monitoring the expression of a number of target
XX polynucleotides.
XX
XX Claim 1, SEQ ID NO 1389; 65pp; English.
XX
XX The invention relates to a combination which, comprises a number of
XX polynucleotide probes comprising a sequence selected from one of the 1490
XX sequences mentioned in the specification. The combination is useful as an
XX array element in a microarray for monitoring the expression of a number
XX of target polynucleotides. The microarray is particularly useful in the
XX diagnosis and treatment of cancer and immunopathology and neuropathology.
XX The microarray is useful in diagnostics and treatment regimens, drug
XX discovery and development, toxicological and carcinogenicity studies,
XX forensic and pharmacogenomics. The microarray is also useful for
XX monitoring progression of diseases and for developing sophisticated
XX profiles for the effects of currently available therapeutic drugs. The
XX combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX and genomic fragments and in research and diagnostic applications. The
XX array can detect changes in expression in a large number of genes coding
XX for different signalling pathway populations which can be used to diagnose
XX various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX and Parkinson's disease. The present sequence represents a polynucleotide
XX probe of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=66500938B1
XX
XX Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0 U; 0 Other;
XX
XX Query Match 10.1%; Score 80.4; DB 10; Length 2372;
XX Best Local Similarity 98.8%; Pred. No. 2.3e-08;
XX Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACATTTTTCCTTTCTTGAATTCATTA 689
XX 1475 CTGAAGAGAGAGGCTGCTCTTTTACTACACATTTTTCCTTTCTTGAATTCATTA 1416
XX
XX 690 CTTCCTTGTAGATTAAGTTCTGT 711
XX 1415 CTTCCTTGTAGATTAAGTTCTTT 1394
XX
XX
XX RESULT 27
XX ADI56587/c
XX ADI56587 standard; DNA; 2372 BP.
XX
XX 22-APR-2004 (first entry)
XX
XX Human polynucleotide probe #1389.
XX
XX Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
XX effector-like polypeptide; cancer; immunopathology; neuropathology;
XX drug development; toxicology; carcinogenicity;
XX signalling pathway polypeptide; adrenal gland; bladder; bone;
XX bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
XX diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
XX dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
XX Homo sapiens.
XX
```

```
PN US2004010136-A1.
XX
XX 15-JAN-2004.
XX
XX 26-NOV-2002; 2002US-00305720.
XX
XX 30-JAN-1998; 98US-00016434.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Sellhammer JU;
XX WPI, 2004-090520/09.
XX
XX New composition comprising polynucleotide probes, useful as array
XX elements in a microarray for monitoring the expression of target
XX polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
XX fragments.
XX
XX Claim 6, SEQ ID NO 1389; 73pp; English.
XX
XX The invention relates to a composition of polynucleotide probes
XX comprising first polynucleotide probes comprising at least a portion of a
XX gene encoding a receptor-like polypeptide, second polynucleotide probes
XX comprising at least a portion of a gene encoding a transducing
XX polypeptide and third polynucleotide probes comprising at least a portion
XX of a gene encoding an effector-like polypeptide. The probes of the
XX composition are useful as array elements in a microarray for monitoring
XX the expression of target polynucleotides. The microarray is useful in the
XX diagnosis and treatment of cancer, an immunopathology or a
XX neuropathology. It can also be used for drug discovery and development,
XX microarrayal and carcinogenicity studies, forensics or pharmacogenomics.
XX Microarrays can also be used for monitoring the progression of diseases
XX that may be associated with the altered expression of signalling pathway
XX polypeptides. The composition can also be used to purify a subpopulation
XX of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
XX is also useful for the diagnosis and treatment of cancer e.g. cancers of
XX the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
XX an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
XX ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
XX epilepsy, Alzheimer's disease or depression. This sequence represents a
XX human polynucleotide probe of the invention. Note: The sequence data for
XX this patent did not form part of the printed specification but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX
XX Sequence 2372 BP; 714 A; 548 C; 519 G; 591 T; 0 U; 0 Other;
XX
XX Query Match 10.1%; Score 80.4; DB 12; Length 2372;
XX Best Local Similarity 98.8%; Pred. No. 2.3e-08;
XX Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACATTTTTCCTTTCTTGAATTCATTA 689
XX 1475 CTGAAGAGAGAGGCTGCTCTTTTACTACACATTTTTCCTTTCTTGAATTCATTA 1416
XX
XX 690 CTTCCTTGTAGATTAAGTTCTGT 711
XX 1415 CTTCCTTGTAGATTAAGTTCTTT 1394
XX
XX
XX RESULT 28
XX ADP45599/c
XX ADP45599 standard; cDNA; 2372 BP.
XX
XX ADP45599;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human MAP kinase MAPK10 (JNK3) cDNA.
XX
XX breast cancer; cytosolic; gene therapy; human; ss; gene; SNP;
XX single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; JNK3A; p493F12;
XX
```


KW p54bAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;
 KM c-Jun N-terminal kinase 3; stress activated protein kinase beta;
 KW chromosome 4q22.1-q23.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 224..1492
 FT /*tag= a
 FT /product= "Human MAP kinase MAPK10 (JNK3) protein"
 FT
 XX
 XX MO2004047623-A2.
 XX
 XX 10-JUN-2004.
 XX
 XX 25-NOV-2003; 2003MO-US037948.
 PF 25-NOV-2002; 2002US-0429136P.
 PR 24-JUL-2003; 2003US-0490234P.
 XX
 XX (SEQU-) SEQUENOM INC.
 PA
 XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
 PI
 XX WPI; 2004-441051/41.
 DR P-PSDB; ADP45606.
 XX
 PT Identifying a subject at risk of breast cancer by detecting the presence
 PT of polymorphic variations in the ICAM, MAPK10, KIA00861, NIMA1 or GALE
 PT regions which are associated with breast cancer in a nucleic acid sample
 PT from a subject.
 XX
 XX Claim 63; SEQ ID NO 9; 289pp; English.
 RS
 CC The invention relates to a novel method for identifying a subject at risk
 CC of breast cancer comprising detecting the presence or absence of one or
 CC more polymorphic variations associated with breast cancer in a nucleic
 CC acid sample from a subject. The method of the invention has cytostatic
 CC applications and may be useful for identifying a subject at risk of
 CC breast cancer, for early diagnosis, prevention and treatment of breast
 CC cancer, possibly via gene therapy, as well as to analyse and predict a
 CC response to a breast cancer treatment and in clinical drug trials. The
 CC current sequence is that of the human MAP kinase MAPK10 (JNK3;JNK3A;
 CC p493F12;p54bAPK MAP kinase;c-Jun kinase 3;JNK3 alpha protein kinase;c-
 CC Jun N-terminal kinase 3;stress activated protein kinase beta) cDNA of the
 CC invention which has been mapped to chromosomal position 4q22.1-q23.
 CC
 CC
 XX
 XX Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
 SQ
 Query Match 10.1%; Score 80.4; DB 12; Length 2372;
 Best Local Similarity 98.8%; Pred. No. 2.3e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
 DB 1475 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
 QY 690 CTTCCTTGTAGATTAAGTTCTGT 711
 DB 1415 CTTCCTTGTAGATTAAGTTCTTT 1394
 RESULT 29
 ADX92938/c
 ID ADX92938 standard; cDNA; 2372 BP.
 XX
 XX ADX92938;
 AC
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX Mitogen-activated protein kinase 10 cDNA.
 DE
 KW cytosolic; gene therapy; human;

KW branching morphogenesis modulating agent; MEM agent; gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX MO2004037990-A2.
 XX
 XX
 XX 06-MAY-2004.
 PD
 XX
 XX 22-OCT-2003; 2003MO-US033549.
 PF 23-OCT-2002; 2002US-0420554P.
 PR 30-DEC-2002; 2002US-0436941P.
 XX
 XX (EXEL-) EXELIXIS INC.
 PA
 XX Plowman GD, Karim PD, Swimmer C, Habeck HA, Koblikz TI;
 PI Schulte-Merker S, Langheinrich U, Scott GM, Trowe T, Vogel AM;
 PI Odenhal JH, Scheel JH, Will TT, Jin Y, Bjerke LM, Hal B;
 PI Adamkiewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
 PI Nicoll M;
 XX
 XX WPI; 2004-365506/34.
 DR P-PSDB; ADX92969.
 XX
 PT Identifying a candidate branching morphogenesis modulating agent for
 PT treating cancer comprises contacting the assay system comprising a MEM
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-
 PT biased activity.
 XX
 XX Example 3; SEQ ID NO 9; 179pp; English.
 RS
 CC The invention describes a method of identifying a candidate branching
 CC morphogenesis modulating (MEM) agent. The method comprises: providing an
 CC assay system comprising a MEM polypeptide or nucleic acid; contacting the
 CC assay system with a test agent under conditions where the system provides
 CC a reference activity, except for the presence of the test agent; and
 CC detecting a test agent-biased activity of the assay system, where a
 CC difference between the test agent-biased activity and the reference
 CC activity identifies the test agent as a candidate branching morphogenesis
 CC modulating agent. Also described are: a method of modulating branching
 CC morphogenesis in a mammalian cell; and a method for diagnosing a disease
 CC in a patient. The method is useful in identifying a candidate branching
 CC morphogenesis modulating agent for preparing a composition for diagnosing
 CC or treating cancer. This sequence encodes a human branching morphogenesis
 CC modulating (MEM) protein.
 CC
 CC
 XX
 XX Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
 SQ
 Query Match 10.1%; Score 80.4; DB 13; Length 2372;
 Best Local Similarity 98.8%; Pred. No. 2.3e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
 DB 1475 CTGAAGAGAGAGCGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
 QY 690 CTTCCTTGTAGATTAAGTTCTGT 711
 DB 1415 CTTCCTTGTAGATTAAGTTCTTT 1394
 RESULT 30
 ADX98578/c
 ID ADX98578 standard; cDNA; 2372 BP.
 XX
 XX ADX98578;
 AC
 XX
 XX 05-MAY-2005 (first entry)
 DT
 XX Human mitogen-activated protein kinase 10 (MAPK10) cDNA.
 DE
 XX SNP detection; breast tumor; endocrine disease;
 KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;

KM Gene therapy; RNA interference; chromosome 4; ss; gene;
KM Mitogen-activated protein kinase 10; Jun N terminal kinase-3; MAPK10.
XX Homo sapiens.
XX MO2005014846-A2.
XX
XX
PD 17-FEB-2005.
XX
PF 27-MAY-2004; 2004MO-US016939.
XX
PR 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
PA (SEQID-) SEQUENOM INC.
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI Hoyal-Wrightson CR;
XX
DR WPI; 2005-163257/17.
DR P-PSDB; ADX98588.
XX
XX
PS Claim 22; SEQ ID NO 11; 617bp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer comprising detecting the presence or absence of a
XX polymorphic variation associated with breast cancer. The method of the
XX invention demonstrates cytostatic activity and may be useful for
XX identifying a risk of, preventing and/or treating breast cancer and
XX cancer metastasis. The methods may be utilized for gene therapy or RNA
XX interference. The current sequence is that of the human mitogen-activated
XX protein kinase 10 (MAPK10) cDNA of the invention which is located at
XX chromosome 4q22.1-q23.
XX
SQ Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
XX
XX
Query Match 10.1%; Score 80.4; DB 14; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGGAGAGAGGCTGCTCTTTACTACACCACTTTTACTCTTCTTGAATTCATTA 689
DB 1475 CTGAAGGAGAGAGGCTGCTCTTTACTACACCACTTTTACTCTTCTTGAATTCATTA 1416
QY 690 CTTCCCTGTAGATAGTTCGT 711
DB 1415 CTTCCCTGTAGATAGTTCGT 1394
RESULT 31
AEG09273/c
ID AEG09273 standard; DNA; 2372 BP.
XX
AC AEG09273;
XX
DT 20-APR-2006 (first entry)
XX
DE Human MAPK10, transcript variant 1 DNA.
XX
XX amyloid-beta precursor protein; pharmaceutical;
KM mitogen activated protein-kinase inhibitor; neurological disease;
KM Alzheimer's disease; degeneration; cognitive disorder; Neuroprotective;
KM Neurotrophic; substrate; mitogen-activated protein kinase 10; MAPK10; ds;
XX gene.
XX Homo sapiens.
XX
FH Key Location/Qualifiers

FT CDS 224..1492
FT /tag= a
FT /product= "mitogen-activated protein kinase 10 (MAPK10),
FT transcript variant 1"
XX
XX
PN MO2005109001-A2.
XX
XX
PD 17-NOV-2005.
XX
PF 12-MAY-2005; 2005MO-EP052182.
XX
PR 12-MAY-2004; 2004US-0570352P.
PR 24-AUG-2004; 2004US-0603948P.
XX
PA (GALA-) GALAPAGOS GENOMICS NV.
PA (LAEN/) LAENEN W.
XX
PI Splitteels KF, Hoffmann M, Merchiers PG;
XX
DR WPI; 2006-231019/24.
DR P-PSDB; AEG09282.
DR REFSEQ; NM_002753.
XX
XX
PT Identifying a compound that inhibits amyloid-beta precursor protein
PT processing in a mammalian cell for treating e.g., Alzheimer's disease by
PT measuring a compound-polypeptide property related to amyloid-beta peptide
PT production.
XX
XX
PS Example 1; SEQ ID NO 9; 84bp; English.
XX
XX This invention describes a novel method of identifying a compound that
XX inhibits the processing of amyloid-beta precursor protein in a mammalian
XX cell. The invention also describes: a) an agent for inhibiting amyloid-
XX beta precursor processing consisting of an antisense polynucleotide, a
XX ribozyme or a small interfering RNA (siRNA), where the agent comprises a
XX nucleic acid sequence complementary to, or engineered from, a naturally-
XX occurring polynucleotide sequence encoding the polypeptide comprising the
XX amino acid sequence of AEG09278 or AEG09279 and b) a pharmaceutical
XX composition comprising the agent for inhibiting amyloid-beta precursor
XX processing or an amyloid-beta precursor processing-inhibiting amount of a
XX mitogen activated protein-kinase inhibitor in admixture with a carrier.
XX The method involves activation of a biological pathway producing an
XX indicator of the processing of amyloid-beta precursor protein e.g. a
XX phosphorylated substrate of a kinase comprising AEG09266-AEG09268. The
XX indicator induces the expression of a reporter e.g. alkaline phosphatase,
XX GFP, eGFP, luciferase or beta-galactosidase in the mammalian cell.
XX The pharmaceutical composition further comprises a label indicating use
XX of the composition for treating or preventing a condition involving
XX cognitive impairment or a susceptibility to the condition. The agent is
XX useful in the manufacture of a medicament for inhibiting the processing
XX of amyloid-beta precursor protein in a subject suffering from or
XX susceptible to the abnormal processing of the protein, or for treating or
XX preventing a condition involving cognitive impairment or a susceptibility
XX to the condition, preferably, Alzheimer's disease. This sequence encodes
XX human mitogen-activated protein kinase 10 (MAPK10), transcript variant 1,
XX a kinase involved in the up-regulation of amyloid-beta 1-42.
XX
SQ Sequence 2372 BP; 714 A; 547 C; 521 G; 590 T; 0 U; 0 Other;
XX
XX
Query Match 10.1%; Score 80.4; DB 15; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.3e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGGAGAGAGGCTGCTCTTTACTACACCACTTTTACTCTTCTTGAATTCATTA 689
DB 1475 CTGAAGGAGAGAGGCTGCTCTTTACTACACCACTTTTACTCTTCTTGAATTCATTA 1416
QY 690 CTTCCCTGTAGATAGTTCGT 711
DB 1415 CTTCCCTGTAGATAGTTCGT 1394
RESULT 32

ACC46216/c
ID ACC46216 standard; cDNA, 2945 BP.
XX
AC ACC46216;
XX
02-JUN-2003 (first entry)
XX
DE Human dithp intracellular signalling protein-encoding cDNA.
XX
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW intracellular signalling; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002MO-US010056.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-028067P.
PR 29-MAR-2001; 2001US-028068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J,
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amehy SR,
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B,
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
XX MPI; 2003-129518/12.
XX
XX P-PSDB; ABR41274.
XX
XX Novel human diagnostic and therapeutic polypeptide useful for identifying
XX test compound which specifically binds to a polypeptide encoded by human
XX diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
XX Claim 2; SEQ ID NO 137; 591pp; English.
XX
XX The invention relates to novel human diagnostic and therapeutic
XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to
XX polynucleotide sequences at least 90% identical to the dithp cDNA
XX sequences of the invention; recombinant vectors, host cells and
XX transgenic organisms comprising a dithp nucleic acid sequence; the
XX recombinant production of DITHP proteins; antibodies specific for DITHP
XX proteins; microarrays comprising dithp nucleic acid sequences; methods of
XX detecting dithp nucleotide and protein sequences; methods of screening
XX for compounds which specifically bind a DITHP protein; and methods of
XX assessing the toxicity of test compounds using a dithp hybridisation
XX probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
XX diagnosis of a wide variety of conditions including cancer and other cell
XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,
XX viral, fungal or parasitic infections; hormonal disorders; metabolic
XX disorders; neurological disorders; gastrointestinal disorders; transport
XX disorders; and connective tissue disorders. They may also be used to
XX screen for modulators of protein activity or gene expression. DITHP
XX proteins can additionally be used in analysis of the proteome of a tissue
XX or cell type and to induce antibodies. The dithp nucleic acids are

CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a dithp cDNA encoding a DITHP protein
CC which has intracellular signalling activity. Note: the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2945 BP; 878 A; 637 C; 671 G; 759 T; 0 U; 0 Other;
Query Match 10.1%; Score 80.4; DB 8; Length 2945;
Best Local Similarity 98.8%; Pred. No. 2.4e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAGAGAGAGGCTGCTTACTACACCATTTTACTTCTTCTGAAATTCATTA 689
DB 1533 CTGAGAGAGAGAGGCTGCTTACTACACCATTTTACTTCTTCTGAAATTCATTA 1474
QY 690 CTTCCTGTAGATAGTTCTGT 711
DB 1473 CTTCCTGTAGATAGTTCTTT 1452
RESULT 33
AD161665/c
ID AD161665 standard; cDNA, 2982 BP.
XX
AC AD161665;
XX
DT 22-APR-2004 (first entry)
XX
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 413797.7.
XX
KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
KW brain disorder.
XX
OS Homo sapiens.
XX
PN US6682888-B1.
XX
PD 27-JUN-2004.
XX
XX 05-MAY-2000; 2000US-00566921.
XX
PF 05-MAY-2000; 2000US-00566921.
XX
PR 05-MAY-2000; 2000US-00566921.
XX
PA (INCY-) INCYTE CORP.
XX
XX Loring JF, Tingley DW, Edwards CW;
XX
XX MPI; 2004-118572/12.
XX
XX New composition comprising cDNAs that are differentially expressed in
XX brain disorders, useful for diagnosing or treating Alzheimer's disease.
XX
XX Claim 1; SEQ ID NO 33; 223pp; English.
XX
XX The invention relates to a new composition comprising AD161633-
XX AD161770 and their complements that are cDNAs differentially expressed in
XX brain disorders. Also included are a high throughput method for detecting
XX differential expression of one or more cDNAs in a sample containing
XX nucleic acids and a high throughput method for screening a library of
XX molecules or compounds to identify a ligand that specifically binds a
XX cDNA. The expression of the each of the cDNAs is downregulated at least
XX two-fold in the brain of the subjects with Alzheimer's disease (AD161633-
XX AD161770) or upregulated at least two fold in Alzheimer's disease
XX (AD161728-AD161770). The composition is useful for diagnosing or treating
XX Alzheimer's disease. The present sequence is a cDNA downregulated at
XX least two-fold in the brain of the subjects with Alzheimer's disease.

SQ Sequence 2982 BP; 868 A; 617 C; 669 G; 781 T; 0 U; 47 Other;
 Query Match 10.1%; Score 80.4; DB 12; Length 2982;
 Best Local Similarity 98.8%; Pred. No. 2.4e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACGTTCTTCTGAAATTCATTA 689
 DB 1570 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACGTTCTTCTGAAATTCATTA 1511
 QY 690 CTTCCTGTAGATTAAGTTCTGT 711
 DB 1510 CTTCCTGTAGATTAAGTTCTTT 1489
 RESULT 34
 AEA43830/c
 ID AEA43830 standard; cDNA; 2982 BP.
 XX
 XX AEA43830;
 AC
 DT 25-AUG-2005 (first entry)
 XX
 DE Human cDNA differentially expressed in brain tissue SEQ ID NO:33.
 KM diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
 KM muscular-gen.; cytotoxic; neuroleptic; nootropic; antidepressant;
 KM anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
 KM immunotherapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2005130171-A1.
 XX
 PD 16-JUN-2005.
 XX
 PF 26-JAN-2004; 2004US-00765700.
 XX
 PR 05-MAY-2000; 2000US-00566921.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Loring JF, Tingley DW, Edwards CM;
 DR WPI; 2005-456990/46.
 XX
 PT Composition useful for diagnosis, staging, treating or monitoring
 PT treatment of a subject with a brain disorder, comprises several cDNAs
 PT that are differentially expressed in brain disorders.
 XX
 PS Claim 1; SEQ ID NO 33; 231pp; English.
 XX
 CC The invention relates to a composition (I) for the diagnosis, staging,
 CC treatment or for the monitoring of treatment of a subject with a brain
 CC disorder. (I) comprises several cDNAs that are differentially expressed
 CC in brain disorders and chosen from any one of 138 nucleotide sequences of
 CC AEA43798-AEA43935, or their complements. Also described: (1) a high
 CC throughput method for detecting differential expression of one or more
 CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II)
 CC selected from AEA43812, AEA43813, AEA43830, AEA43855, AEA43856,
 CC AEA43883 and AEA43923; (3) an expression vector (III) containing (II);
 CC (4) a host cell (IV) containing (III); (5) a protein (V) produced using
 CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful
 CC for a high throughput method of screening a library of molecules or
 CC compounds to identify a ligand which specifically binds a cDNA, where the
 CC method involves combining (I) with the library of molecules or compound
 CC under conditions to allow specific binding and detecting specific binding
 CC between each cDNA and a molecule or compound. (IV) is useful for
 CC producing a protein, which involves culturing (IV) under conditions for
 CC the expression of the protein and recovering the protein from the
 CC culture. (V) is useful for high throughput method for screening a library
 CC of molecules or compounds to identify a ligand which specifically binds
 CC (V), where the method involves combining (V) or its portion with the

CC library of molecules or compound under conditions to allow specific
 CC binding and detecting specific binding between (V) and a molecule or
 CC compound. (V) is useful for purifying a ligand from a sample, which
 CC involves combining (V) or its portion with the sample under conditions to
 CC allow specific binding, recovering the bound protein and separating the
 CC protein from ligand. (V) is also useful for producing an antibody, which
 CC involves immunizing an animal with (V) or its portion under conditions to
 CC elicit an antibody response, isolating animal antibodies and screening
 CC the isolated antibodies with the protein. (II) is useful in gene therapy
 CC for the treatment or prevention of conditions and disorders associated
 CC with immune response. The present sequence represents a human cDNA
 CC sequence which is differentially expressed in brain tissues, which is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 2982 BP; 868 A; 617 C; 669 G; 781 T; 0 U; 47 Other;
 Query Match 10.1%; Score 80.4; DB 14; Length 2982;
 Best Local Similarity 98.8%; Pred. No. 2.4e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACGTTCTTCTGAAATTCATTA 689
 DB 1570 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACGTTCTTCTGAAATTCATTA 1511
 QY 690 CTTCCTGTAGATTAAGTTCTGT 711
 DB 1510 CTTCCTGTAGATTAAGTTCTTT 1489
 RESULT 35
 AAH47044/c
 ID AAH47044 standard; DNA; 8749 BP.
 XX
 XX AAH47044;
 AC
 DT 29-OCT-2001 (first entry)
 XX
 DE Nucleotide sequence of pFastFind-Jnk3 vector.
 KM IRES; internal ribosome initiation sequence; promoter; surface marker;
 KM label protein; membrane protein; ds.
 XX
 OS Synthetic.
 XX
 PN WO200157212-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US003411.
 XX
 PR 02-FEB-2000; 2000US-0179893P.
 XX
 PA (ICON-) ICONIX PHARM INC.
 XX
 PI Jarnigan K, Zhou H;
 DR WPI; 2001-476284/51.
 XX
 PT Polynucleotide for rapid isolation of candidate eukaryotic cell clones
 PT comprises a promoter, a test gene, an IRES sequence and a surface marker.
 XX
 PS Example; Page 32-37; 32pp; English.
 XX
 CC The invention relates to a polynucleotide (I) comprising: (a) a
 CC regulatable promoter; (b) a test gene; (c) an IRES sequence; and (d) a
 CC surface marker coding sequence comprising a secretion signal sequence, a
 CC detectable label protein and a membrane protein where expression of the
 CC test gene also results in expression of the surface marker. A method is
 CC provided for identifying a host cell that exhibits regulated expression
 CC of a test gene complex that comprises (a) providing more than one host
 CC cell; (b) inducing the promoter; and (c) selecting a host cell that
 CC displays the surface marker on its surface. (I), the host cell and the
 CC method are useful for the rapid isolation of candidate eukaryotic cell

CC clones in which a query gene is regulated by exogenous application of an
CC appropriate stimulus. The present sequence represents the nucleotide
CC sequence of a pFastbind-Jmk3 vector

SO Sequence 8749 BP; 2128 A; 2329 C; 2287 G; 2005 T; 0 U; 0 Other;

Query Match 10.1%; Score 80.4; DB 4; Length 8749;

Best Local Similarity 98.8%; Pred. No. 3e-08; Mismatches 1; Indels 0; Gaps 0;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 630 CTGAAGGAGAGGCTGCTCTTCTTACTACACCATTTTGTCTTCTTCTGAATTCATTA 689

Db 1781 CTGAAGGAGAGGCTGCTCTTCTTACTACACCATTTTGTCTTCTTCTGAATTCATTA 1722

Qy 690 CTTCCTGTAGATAGTCTGT 711

Db 1721 CTTCCTGTAGATAGTCTGT 1700

RESULT 36

AAT10640/c

ID AAT10640 standard; cDNA; 1975 BP.

AC AAT10640;

DT 26-APR-1996 (first entry)

DE Stress activated protein kinase p54 beta-I cDNA.

KM Stress activated protein kinase; SAPK; p54 beta-I; antibody;

KM Inflammation; hypoxia; heat stress; ss.

OS Rattus sp.

FX Key Location/Qualifiers

FT CDS 364..1644

FT /*CDS= a

PN CA2148898-A.

PD 10-NOV-1995.

PF 08-MAY-1995; 95CA-02148898.

PR 09-MAY-1994; 94US-00240014.

PA (GEHO) GEN HOSPITAL CORP.

PA (ONTA-) ONTARIO CANCER INST.

PI Kyriakis JM, Avruch J, Banerjee P, Woodgett JR;

DR WFI, 1996-106355/12.

XX DNA encoding recombinant p54 stress activated protein kinase - and

PT related antibodies, useful for treating inflammation, hypoxia and heat

PT stress, and for drug screening.

PS Claim 20; Page 44-45; 68pp; English.

XX A cDNA clone (AAT10640) was obtd. that codes for rat proline-directed

CC stress-activated protein kinase (SAPK) p54 beta-I (AAR89410). This cDNA,

CC and others (see AAT10638-39 and AAT10641-42) coding for p54 alpha-I,

CC alpha-II, beta-II and gamma (AAR89408-9 and AAR89411-12), were isolated

CC from a rat brain cDNA library following PCR amplification using primers

CC based on p54 tryptic peptides obt. from a cycloheximide-treated rat

Db 1505 GCACCTGAAGTGAAGGCTGCTCTTACTACACCATTTTGTCTTCTTCTGAATTC 1446

Qy 686 ATTACTCTCTGTAGATAGTCTGT 711

Db 1445 ATTACTCTCTGTAGATAGTCTGT 1420

RESULT 37

ABL88414/c

ID ABL88414 standard; cDNA; 1975 BP.

AC ABL88414;

DT 16-MAY-2002 (first entry)

DE Pain regulated cDNA sequence 57.

KM Pain; analgesic; gene therapy; neurological disorder;

KM neurodegenerative disease; gene; ss.

OS Rattus sp.

FX WO200212338-A2.

PD 14-FEB-2002.

PF 03-AUG-2001; 2001WO-EP009011.

PR 03-AUG-2000; 2000DE-01037759.

PA (CHEF) GRUNENTHAL GMBH.

PI Gallen C, Wetzel S, Wehne E, Schaefer MK;

DR WFI; 2002-257469/30.

XX P-PSDB; ABB85009.

PT Identifying pain-regulating compounds, useful for treating chronic pain

PT and for diagnosis, by measuring binding of compounds to specific peptides

PT and proteins.

PS Claim 1; Fig 34; 213pp; German.

XX The invention relates to identifying pain-regulating substances (A)

CC comprises (i) incubating a test substance with a cell (or preparation

CC from it) that has synthesised a peptide or protein (B) and (ii) measuring

CC either binding of the test substance to (B) or some functional parameter

CC that is altered by this binding. The method is useful for identifying

CC pain-regulating substances (A) with analgesic activity. (A) along with

CC nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-

CC ABB85037) that interact with (A); (B); vectors containing the nucleic

CC acid; antibodies against (B); cells that express (B) and agents that bind

CC to (B); are all useful for treating pain, particularly chronic pain,

CC including use in gene therapy. The same materials can also be used for

CC diagnosis, e.g. of neurological and neurodegenerative diseases. The

CC present sequence is that of a polynucleotide of the invention

SO Sequence 1975 BP; 556 A; 506 C; 488 G; 425 T; 0 U; 0 Other;

Query Match 8.3%; Score 66.8; DB 6; Length 1975;

Best Local Similarity 86.0%; Pred. No. 2.8e-05; Mismatches 12; Indels 0; Gaps 0;

Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGGAGGCTGCTCTTCTTACTACACCATTTTGTCTTCTTCTGAATTC 685

Db 1505 GCACCTGAAGTGAAGGCTGCTCTTACTACACCATTTTGTCTTCTTCTGAATTC 1446

Qy 686 ATTACTCTCTGTAGATAGTCTGT 711

Db 1445 ATTACTCTCTGTAGATAGTCTGT 1420

Qy 626 GTACCTGAAGGAGGCTGCTCTTCTTACTACACCATTTTGTCTTCTTCTGAATTC 685

Db 1505 GCACCTGAAGTGAAGGCTGCTCTTACTACACCATTTTGTCTTCTTCTGAATTC 1446

```

RESULT 38
ABL88413/C
ID ABL88413 standard; cDNA; 1240 BP.
XX
XX ABL88413;
AC
XX
XX 16-MAY-2002 (first entry)
DT
XX
XX Pain regulated cDNA sequence 56.
DE
XX
XX Pain; analgesic; gene therapy; neurological disorder;
KM
XX neurodegenerative disease; gene; ss.
XX
XX Mus sp.
OS
XX
XX WO200212338-A2.
XX
XX 14-FEB-2002.
PD
XX
XX 03-AUG-2001; 2001MO-EP009011.
PF
XX
XX 03-AUG-2000; 2000DE-01037759.
PR
XX
XX (CHEF ) GRUENENTHAL GMBH.
XX
XX G11len C, Wetzel S, Wnendt S, Weine E, Schaefer MK;
PI
XX WPI; 2002-257469/30.
DR
XX P-PSDB; ABB85008.
XX
XX
XX Identifying pain-regulating compounds, useful for treating chronic pain
PT and for diagnosis, by measuring binding of compounds to specific peptides
PT and proteins.
XX
XX Claim 1; Fig 34; 213pp; German.
XX
XX The invention relates to identifying pain-regulating substances (A);
XX comprises (i) incubating a test substance with a cell (or preparation
XX from it) that has synthesised a peptide or protein (B) and (ii) measuring
XX either binding of the test substance to (B) or some functional parameter
XX that is altered by this binding. The method is useful for identifying
XX pain-regulating substances (A) with analgesic activity. (A) along with
XX nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-
XX ABB85037) that interact with (A); (B); vectors containing the nucleic
XX acid; antibodies against (B); cells that express (B) and agents that bind
XX to (B); are all useful for treating pain, particularly chronic pain;
XX including use in gene therapy. The same materials can also be used for
XX diagnosis, e.g. of neurological and neurodegenerative diseases. The
XX present sequence is that of a polynucleotide of the invention
XX
XX
SQ Sequence 1240 BP; 359 A; 299 C; 317 G; 265 T; 0 U; 0 Other;
Query Match 8.2%; Score 66; DB 6; Length 1240;
Best Local Similarity 87.8%; Pred. No. 3.8e-05;
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTAACTCTTCTTCTGAAATCATTA 689
DB 1201 CTGAAGGCGAGGCGCTGCTTTGACCTAGCCATTCTTCTTCTGAGTTCAATTA 1142
QY 690 CTTCCTTGTAGATAGTTCTGT 711
DB 1141 CTTCCTTGTAGATAGTTCTTT 1120

```

```

DE Stress activated protein kinase p54 beta-II cDNA.
XX
XX Stress activated protein kinase; SAPK; p54 beta-II; antibody;
KM inflammation; hypoxia; heat stress; ss.
XX
XX Rattus sp.
OS
XX
XX Key Location/Qualifiers
XX CDS 364..1644
XX FT /*tag= a
XX FT misc_difference 1549
XX FT /note= "base 1549 is unclear in the specification,
XX FT probably C or G"
XX FT misc_difference 1550
XX FT /*tag= C
XX FT /note= "base 1550 is unclear in the specification,
XX FT probably C or G"
XX
XX CA2148898-A.
XX
XX 10-NOV-1995.
PD
XX
XX 08-MAY-1995; 95CA-02148898.
PF
XX
XX 09-MAY-1994; 94US-00240014.
PR
XX
XX (GENO ) GEN HOSPITAL CORP.
XX (ONTA-) ONTARIO CANCER INST.
XX
XX Kyriakis JM, Avruch J, Banerjee P, Woodgett JR;
PI
XX WPI; 1996-106355/12.
DR
XX P-PSDB; AAR89411.
XX
XX
XX DNA encoding recombinant p54 stress activated protein kinase - and
XX PT related antibodies, useful for treating inflammation, hypoxia and heat
XX PT stress, and for drug screening.
XX
XX Claim 21; Page 46-47; 68pp; English.
XX
XX A cDNA clone (AAT10641) was obt'd. that codes for rat proline-directed
XX stress-activated protein kinase (SAPK) p54 beta-II (AAR89411). This cDNA,
XX CC and others (see AAT10638-40 and AAT10642) coding for p54 alpha-I, alpha-
XX CC II, beta-I and gamma (AAR89408-10 and AAR89412), were isolated from a rat
XX CC brain cDNA library following PCR amplification using primers based on p54
XX CC tryptic peptides obt. from a cycloheximide-treated rat
XX
XX
SQ Sequence 1986 BP; 559 A; 510 C; 488 G; 427 T; 0 U; 2 Other;
Query Match 8.1%; Score 64.4; DB 2; Length 1986;
Best Local Similarity 86.6%; Pred. No. 9.7e-05;
Matches 71; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTAACTCTTCTTCTGAAATCATTA 689
DB 1507 CTGAAGGTAGAGGCTGCGCTTTGACCTAGCCGCTTCTTCTTCTGAGTTCAATTA 1448
QY 690 CTTCCTTGTAGATAGTTCTGT 711
DB 1447 CTTCCTTGTAGATAGTTCTTT 1426

```

```

RESULT 39
AAT10641/C
ID AAT10641 standard; cDNA; 1986 BP.
XX
XX AAT10641;
AC
XX
XX 26-APR-1996 (first entry)
DT
XX
XX

```

```

RESULT 40
AAT10642/C
ID AAT10642 standard; cDNA; 1408 BP.
XX
XX AAT10642;
AC
XX
XX 26-APR-1996 (first entry)
DT
XX
XX Stress activated protein kinase p54 gamma cDNA.
DE
XX
XX

```

KW Stress activated protein kinase; SAPK; p54 gamma; antibody; inflammation;
 KM hypoxia; heat stress; ss.
 XX Rattus sp.
 OS
 XX Key Location/Qualifiers
 FH CDS 176..1408
 FT /*tag= a
 XX
 XX CA2148898-A.
 XX
 XX 10-NOV-1995.
 XX
 XX 08-MAY-1995; 95CA-02148898.
 XX
 XX 09-MAY-1994; 94US-00240014.
 XX
 XX (GENO) GEN HOSPITAL CORP.
 XX (ONTA-) ONTARIO CANCER INST.
 XX
 XX Kyriakis JM, Avruch J, Banerjee P, Woodgett JR;
 XX WPI; 1996-106355/12.
 XX P-PSDB; AAR89412.
 XX
 XX DNA encoding recombinant p54 stress activated protein kinase - and
 PT related antibodies, useful for treating inflammation, hypoxia and heat
 PT stress, and for drug screening.
 XX
 XX Claim 22; Page 47-48; 68pp; English.
 XX
 CC A cDNA clone (AA110642) was obtd. that codes for rat proline-directed
 CC stress-activated protein kinase (SAPK) p54 gamma (AAR89412). This cDNA,
 CC and others (see AA110658-41) coding for p54 alpha-I, alpha-II, beta-I and
 CC beta-II (AAR89408-11), were isolated from a rat brain cDNA library
 CC following PCR amplification using primers based on p54 cryptic peptides
 CC obt. from a cycloheximide-treated rat
 CC
 XX
 XX Sequence 1408 BP; 408 A; 310 C; 339 G; 351 T; 0 U; 0 Other;
 SQ
 Query Match 6.3%; Score 50.8; DB 2; Length 1408;
 Best Local Similarity 74.4%; Pred. No. 0.11;
 Matches 64; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 626 GTACCTGAAGAGAGAGCTGCTTTACTACACCAATTTTTCCTTCTTGAATTC 685
 DB 1317 GCACCTTAAGAGAGAGCGCTGCTCTATAGAGCCATTCTTAGTCCCTCCAAATCC 1258
 QY 686 ATTACTCTCTGTGATTAAGTTCTGT 711
 DB 1257 ATGACCTCTGTATATCATGTTCTTT 1232
 RESULT 41
 ABT09489/c
 ID ABT09489 standard; DNA; 580 BP.
 XX
 AC ABT09489;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE Phase-1 Rat CT gene SEQ ID No 577.
 XX
 KM Rat; toxicity study; rat toxic response gene; toxicological response;
 KM drug development; phase-1 rat CT gene; ds.
 XX
 OS Rattus sp.
 XX
 XX WO200266682-A2.
 XX
 XX 29-AUG-2002.
 XX
 XX 29-JAN-2002; 2002WO-US002935.
 PF

XX
 PR 29-JAN-2001; 2001US-0264933P.
 PR 26-JUL-2001; 2001US-0308161P.
 XX
 XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 PA
 XX
 PI Farris G, Hicken SH, Farr SB;
 XX
 XX WPI; 2002-674961/72.
 XX
 XX
 XX Evaluating the toxicity of an agent, useful in drug development or in
 PT determining toxicological responses to a new drug, by determining the
 PT expression of rat toxicologically relevant genes in the test animal in
 PT response to the test agent.
 XX
 XX
 XX Disclosure; Page 247; 388pp; English.
 XX
 CC The invention relates to a method used for evaluating the toxicity of an
 CC agent comprising determining the expression of a rat toxic response
 CC gene(s) in the test animal in response to the agent. The method is useful
 CC in drug development, particularly for conducting toxicity studies and
 CC analysis before a new drug or compound is approved for human consumption
 CC or use. The method is also useful in determining toxicological responses
 CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT
 CC gene of the invention
 CC
 XX
 XX Sequence 580 BP; 170 A; 129 C; 145 G; 125 T; 0 U; 11 Other;
 SQ
 Query Match 6.2%; Score 49.4; DB 6; Length 580;
 Best Local Similarity 74.7%; Pred. No. 0.19;
 Matches 62; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 QY 629 CCTGAAGAGAGAGAGCTGCTTTACTACACCAATTTTTCCTTCTTGAATTCAT 688
 DB 494 CCTTAAGAGAGAGAGCGCTGCTCTATAGAGCCATTCTTAGTCCCTCCAAATCATG 435
 QY 689 ACTTCTCTGTGATTAAGTTCTGT 711
 DB 434 ACCTCTCTGTATATCATGTTCTTT 412
 RESULT 42
 ADG30924/c
 ID ADG30924 standard; DNA; 580 BP.
 XX
 AC ADG30924;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Liver toxicity predictive DNA 104.
 XX
 XX Liver toxicity; Norway rat; 24 hour combo All; ds.
 XX
 XX Unidentified.
 OS
 XX
 XX WO2003085083-A2.
 XX
 XX 16-OCT-2003.
 PD
 PF 01-APR-2003; 2003WO-US010141.
 XX
 PR 01-APR-2002; 2002US-0369287P.
 XX
 XX (PHAS-) PHASE 1 MOLECULAR TOXICOLOGY.
 PA
 XX Kler L, Nolan TD, Sankar U, Derbel M;
 PI
 XX WPI; 2003-804300/75.
 XX
 XX Predicting the liver toxicity of an agent to an individual by using the
 PT test expression profile with a set of reference expression profiles in a
 PT Predictive Model to determine whether the agent will reduce liver
 PT toxicity in the individual.
 PT

XX Claim 2; Page 168; 379pp; English.
XX
XX The invention relates to a novel method for predicting the liver toxicity
CC of an agent to an individual comprising obtaining a biological sample
CC from an individual treated with the agent, measuring the expression of
CC one or more liver toxicity predictive genes in the sample and using the
CC test expression profile with a set of reference expression profiles in a
CC predictive model to determine whether the agent will reduce liver
CC toxicity in the individual. The method of the invention may be useful for
CC predicting the liver toxicity of an agent to an individual. The current
CC sequence is that of the liver toxicity predictive DNA of the invention
CC which represents a 24 hour combo All gene.
XX
SQ Sequence 580 BP; 170 A; 129 C; 145 G; 125 T; 0 U; 11 Other;
Query Match 6.2%; Score 49.4; DB 10; Length 580;
Best Local Similarity 74.7%; Pred. No. 0.19;
Matches 62; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY 629 CCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTGAATTCATT 688
DB 494 CCTAAAGAGAGAGCGCTGCCCTCTATGACGCCATTTAGTTGCTCTCAATCCATG 435
OY 689 ACTTCCTGTAGATAGTTCGT 711
DB 434 ACCTCCTGTATATCATGTTCTTT 412
RESULT 43
ADG45512/c
ID ADG45512 standard; DNA; 580 BP.
XX
XX ADG45512;
AC
XX 26-FEB-2004 (first entry)
XX
XX Liver inflammatory predictive gene related DNA sequence.
DE
XX liver; liver toxicity; liver toxicity predictive gene;
KW liver inflammation predictive gene; inflammation; gene; ds; rat.
XX
XX Rattus norvegicus.
OS
XX
XX MO2003095624-A2.
PN
XX 20-NOV-2003.
PD
XX 09-MAY-2003; 2003MO-US014832.
PF
XX 10-MAY-2002; 2002US-0379831P.
PR
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
PA
XX Klier L, Nolan TD, Sankar U, Derbel M,
PI
XX MPI; 2004-042456/04.
XX
XX
XX Predicting the liver toxicity in an individual to an agent by measuring
PT the expression of one or more liver toxicity predictive genes in the
PT sample from the individual treated with the agent.
XX
XX
XX Claim 7; Fig 4; 336pp; English.
XX
XX The present invention describes a method for predicting the liver
CC toxicity in an individual to an agent. The method comprises: (a)
CC obtaining a biological sample from the individual treated with the agent;
CC (b) measuring the expression of one or more liver toxicity predictive
CC genes in the sample; and (c) using the test expression profile with a set
CC of reference expression profiles in a Predictive Model to determine
CC whether the agent will induce liver toxicity in the individual. Also
CC described: (1) predicting the liver toxicity of an agent using an in
CC vitro system; (2) predicting the liver toxicity in a biological sample

CC from an individual, in vitro cell cultures or explants to an agent via a
CC programmable machine; (3) a computer program product for enabling a
CC computer to perform Predictive Model analysis for liver toxicity on a
CC biological sample from an individual, in vitro cell cultures or explants
CC to an agent; (4) a computer system adopted to predict liver toxicity in a
CC biological system from an individual, in vitro cell cultures or explants
CC to an agent; (5) a computer program product for predicting liver toxicity
CC from a test sample expression profile; (6) mining genes predictive of
CC liver toxicity; (7) an integrated system for predicting liver toxicity;
CC and (8) identifying one or more liver inflammation predictive genes. The
CC method is useful for predicting the liver toxicity in an individual to an
CC agent. The present sequence represents a liver toxicity predictive gene
CC sequence that represents a 24 hour combo 3 gene, which is specifically
CC claimed in the exemplification of the present invention.
XX
SQ Sequence 580 BP; 170 A; 129 C; 145 G; 125 T; 0 U; 11 Other;
Query Match 6.2%; Score 49.4; DB 12; Length 580;
Best Local Similarity 74.7%; Pred. No. 0.19;
Matches 62; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY 629 CCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTTTCTTCTGAATTCATT 688
DB 494 CCTAAAGAGAGAGCGCTGCCCTCTATGACGCCATTTAGTTGCTCTCAATCCATG 435
OY 689 ACTTCCTGTAGATAGTTCGT 711
DB 434 ACCTCCTGTATATCATGTTCTTT 412
RESULT 44
ADR91158/c
ID ADR91158 standard; cDNA; 580 BP.
XX
XX ADR91158;
AC
XX 16-DEC-2004 (first entry)
XX
XX Spleen necrosis predictive cDNA sequence, SEQ ID NO 114.
DE
XX altered expression; toxic response; spleen; toxicity; lymphoid; gene; ss.
KW
XX
XX Unidentified.
OS
XX
XX MO2004083402-A2.
PN
XX 30-SEP-2004.
PD
XX 17-MAR-2004; 2004MO-US008371.
PF
XX 17-MAR-2003; 2003US-0455443P.
PR
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
PA
XX Sankar U, Klier L, Derbel M, Nolan T,
PI
XX MPI; 2004-691048/67.
XX
XX
XX New composition comprises cDNAs useful for detecting altered expression
PT of genes in a toxic response of the spleen or for predicting toxic
PT responses to one or more agents including lymphoid tissue types or other
PT species.
XX
XX
XX Claim 1; SEQ ID NO 114; 249pp; English.
XX
XX The invention relates to a novel composition comprising cDNAs for use in
CC detecting the altered expression of genes in a toxic response of the
CC spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348)
CC or their complete complements. The invention further comprises:
CC monitoring the treatment of compound toxicity in a sample; predicting the
CC spleen toxicity in an individual to an agent; predicting the spleen
CC toxicity of an agent using an in vitro system; a computer program product
CC for predicting spleen toxicity from an expression profile of nucleic

PN US2003190735-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 18-MAY-2001; 2001US-00861012.
 XX
 PR 19-JUL-1993; 93US-00094533.
 PR 25-MAR-1994; 94US-00220602.
 PR 18-JUL-1994; 94US-00276860.
 PR 19-MAY-1995; 95US-0044393.
 PR 13-FEB-1997; 97US-00799913.
 PR 08-SEP-1998; 98US-00150201.
 PR 14-DEC-1999; 99US-00461649.
 XX
 PA (KARI/) KARIN M.
 PA (HIBI/) HIBI M.
 PA (LINA/) LIN A.
 XX
 PI Karin M, Hibi M, Lin A;
 DR WPI; 2003-044275/78.
 DR P-PSDB; ADJ64021.
 XX
 PT New polynucleotide encoding a c-Jun N-terminal kinase (JNK), and the
 PT encoded polypeptide, useful for (identifying compounds for) treating e.g.
 PT cancer, psoriasis, rheumatoid arthritis, or septic shock.
 XX
 PS Claim 7; SEQ ID NO 17; 50pp; English.
 XX
 CC This invention relates to a novel polynucleotide encoding a c-Jun N-
 CC terminal kinase that phosphorylates the c-Jun N-terminal activation
 CC domain. The polynucleotide sequence of the invention may have cytostatic,
 CC immunosuppressive, dermatological, anti-inflammatory, cardiant,
 CC antirheumatic, antiarthritic, anti-HIV, respiratory-gen, antipsoriatic,
 CC vasotropic, antibacterial, antileukemic activities. Also disclosed in the
 CC invention are modulators of the activity or expression of the c-Jun N-
 CC terminal kinase (JNK) such as competitive inhibitor peptides, antibodies,
 CC and sense or antisense polynucleotides which are useful for treating cell
 CC proliferative disorders associated with JNK. These include cancers such
 CC as colon cancer, renal cell carcinoma, prostate cancer, and non-small
 CC cell carcinoma, and non-malignant or immunological-related cell
 CC proliferative diseases, such as psoriasis, pemphigus vulgaris, Behçet's
 CC syndrome, acute respiratory distress syndrome (ARDS), ischemic heart
 CC disease, post-dialysis syndrome, leukemia, rheumatoid arthritis, AIDS,
 CC vasculitis, septic shock, and other types of inflammation or lipid
 CC histiocytosis. The polypeptide of the invention may be useful in a
 CC screening method for identifying molecules which modulate its activity
 CC which are potentially useful as therapeutics. The present sequence
 CC represents a DNA sequence encoding the JNK2 protein used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 1765 BP; 539 A; 356 C; 396 G; 474 T; 0 U; 0 Other;
 Query Match 6.0%; Score 48.4; DB 10; Length 1765;
 Best Local Similarity 74.4%; Pred. No. 0.41; Mismatches 0; Gaps 0;
 Matches 61; Conservative 0; Indels 21; Indels 0; Gaps 0;
 QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCATTA 689
 DB 1196 CTGCATCTGAGAGGCTGATCTTTTACACACCATTTGCTTCTTCCCAATCATGA 1137
 QY 690 CTTCCTGTGATGAATTCGT 711
 DB 1136 CTTCCTGTGAATTAATGCTCTTT 1115

DT 13-OCT-1995 (first entry)
 XX
 DE JNK2 Oncoprotein polypeptide kinase coding sequence.
 XX
 KM Oncoprotein; polypeptide kinase; JNK; c-Jun; AP-1; Leukemia;
 KM prostate cancer; lung cancer; colon cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FH CDS 59..1336
 FT /*tag= a
 FT /product= "Oncoprotein protein kinase."
 XX
 XX W05033323-A1.
 XX
 PD 02-FEB-1995.
 XX
 PF 18-JUL-1994; 94WO-US008119.
 XX
 PR 19-JUL-1993; 93US-00094533.
 PR 25-MAR-1994; 94US-00220602.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (UYMA-) UNIV MASSACHUSETTS MEDICAL SCHOOL.
 XX
 PI Karin M, Davis R, Hibi M, Lin A, Derjard B;
 DR WPI; 1995-075186/10.
 DR P-PSDB; AAR70768.
 XX
 PT Oncoprotein protein kinase, JNK - useful for regulating c-Jun activity
 PT and gene expression in cells.
 XX
 PS Claim 57; Fig 28; 143pp; English.
 XX
 CC JNK1 (See AAR70767) and JNK2 phosphorylate the c-Jun N-terminal
 CC activation domain which affect gene expression from AP-1 sites. The 2
 CC protein kinases allow the detection of the level of specific kinase
 CC activity associated with activation of c-Jun and AP-1. Cell proliferative
 CC disorders associated with JNK can be treated by administering a
 CC therapeutically effective amount of a reagent which modulates JNK
 CC activity. Disorders such as leukemia, cancers of prostate, lung (non-
 CC small cell) and colon. (updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1780 BP; 541 A; 363 C; 402 G; 474 T; 0 U; 0 Other;
 Query Match 6.0%; Score 48.4; DB 2; Length 1780;
 Best Local Similarity 74.4%; Pred. No. 0.41; Mismatches 0; Gaps 0;
 Matches 61; Conservative 0; Indels 21; Indels 0; Gaps 0;
 QY 630 CTGAGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTGAATTCATTA 689
 DB 1196 CTGCATCTGAGAGGCTGATCTTTTACACACCATTTGCTTCTTCCCAATCATGA 1137
 QY 690 CTTCCTGTGATGAATTCGT 711
 DB 1136 CTTCCTGTGAATTAATGCTCTTT 1115

RESULT 48
 ADA26313/C
 ID ADA26313 standard; cDNA; 1780 BP.
 XX
 AC ADA26313;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE cDNA encoding c-Jun N-terminal kinase 2, JNK2.
 XX
 KM immunological disorder; non-malignant cell-proliferative disorder;
 KM leukemia; organ related malignancy; acute inflammation;
 KM c-Jun N-terminal kinase 2; JNK 2; immunopathological disorder;

ID	ACa62801/C	standard; DNA; 1780 BP.
XX	ACa62801;	
XX	21-AUG-2003	(first entry)
XX	Human c-Jun N-terminal kinase, JNK2, cDNA.	
XX	Human, JNK2; cell proliferative disorder; serine kinase; ss; gene;	
XX	threonine kinase; psoriasis; pemphigus vulgaris; Behcet's syndrome;	
XX	acute respiratory distress syndrome; ARDS; ischaemic heart disease;	
XX	leukaemia; rheumatoid arthritis; AIDS; vasculitis; septic shock; cancer;	
XX	c-Jun N-terminal kinase.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	59..1333
XX	FT	/*tag= a
XX	FT	/product= "JNK2"
XX	US200304788-A1.	
XX	06-MAR-2003.	
XX	18-MAY-2001; 2001US-00861098.	
XX	19-JUL-1993; 93US-00094533.	
XX	25-MAR-1994; 94US-00220602.	
XX	18-JUL-1994; 94US-00276860.	
XX	19-MAY-1995; 95US-00444393.	
XX	13-FEB-1997; 97US-00799913.	
XX	08-SEP-1998; 98US-00150201.	
XX	14-DEC-1999; 99US-00461649.	
XX	(KARI/) KARIN M.	
XX	(HIBI/) HIBI M.	
XX	(LINA/) LIN A.	
XX	Karin M, Hibi M, Lin A;	
XX	WPI; 2003-479738/45.	
XX	P-PSDB; ABU62138.	
XX	Identifying a composition useful to treat a cell proliferative disorder,	
XX	comprises incubating the composition and a serine/threonine kinase or	
XX	polynucleotide encoding the kinase and measuring the effect of the	
XX	composition on the kinase.	
XX	Claim 3; Page 32-34; 50pp; English.	
XX	The invention relates to a method of identifying a composition useful for	
XX	treating a proliferative disorder, affecting a kinase having serine and	
XX	threonine kinase activity and phosphorylating a c-Jun N-terminal	
XX	activation domain. The method is useful for identifying a composition	
XX	which is useful for treating a cell proliferative disorder, where the	
XX	effect is inhibition or stimulation of the kinase, and the composition is	
XX	an immunosuppressing agent. The composition identified by the above	
XX	method, is useful for treating a cell proliferative disorder e.g. cancer,	
XX	psoriasis, pemphigus vulgaris, Behcet's syndrome, acute respiratory	
XX	distress syndrome (ARDS), ischaemic heart disease, leukaemia, rheumatoid	
XX	arthritis, AIDS, vasculitis and septic shock. The present sequence	
XX	represents the human c-Jun N-terminal kinase, JNK2, cDNA	
XX	Sequence 1780 BP; 541 A; 359 C; 402 G; 478 T; 0 U; 0 Other;	
XX	Query Match	6.0%; Score 48.4; DB 9; Length 1780;
XX	Best Local Similarity	74.4%; Pred. No. 0.41;
XX	Matches	61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGGCTGCTTTTACTACACATTTTGTCTTCTTGAATTCATTA 689
 DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACATCTTGTCTTCTTCCCAATCCATGA 1137
 QY 690 CTTCCTTGATAGATAGTCTGT 711
 DB 1136 CTTCCTTGATAGATAGTCTGT 1115

RESULT 50

AAA48656/c

ID AAA48656 standard; DNA; 1782 BP.

AC AAA48656;

DT 20-SEP-2000 (first entry)

DE Human JNK2 DNA.

XX Antisense; E-selectin; TNF alpha; cell adhesion; human;
 KM tumour necrosis factor alpha; phosphorothioate; methoxyethoxy; sepsis;
 KM rheumatoid arthritis; inflammatory; immune disease;
 KM inflammatory bowel disease; allergic contact dermatitis; psoriasis;
 KM diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
 KM immunosuppressive; antipsoriatic; antidiabetic; antithyroid; cytostatic;
 KM dermatological; antiallergic; Ha-ras; c-raf; c-Jun N-terminal kinase;
 KM JNK; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 59..1333

FT /*tag= a

FT /product= "JNK2"

PN W0200034303-A1.

PD 15-JUN-2000.

PF 08-DEC-1999; 99W0-US028965.

PR 10-DEC-1998; 98US-00209668.

PA (ISIS-) ISIS PHARM INC.

PI Monia BP, Xu XS;

DR WPI; 2000-423367/36.

DR P-PSDB; AAY94503.

PT Modulating cell adhesion molecule expression for treating immune or
 PT inflammatory diseases involves treating cell with specific inhibitor of
 PT Tumor Necrosis Factor alpha signaling molecule.
 PS Example 2; Page 88-90; 100pp; English.

CC A novel method for modulating cell adhesion molecule expression involves
 CC antisense inhibition of a tumour necrosis factor (TNF) alpha signaling
 CC molecule. In the method TNF alpha signaling molecules Ha-ras, c-raf and
 CC c-Jun N-terminal kinase (JNK)2 were inhibited by antisense
 CC oligonucleotides. In addition an antisense oligonucleotide to the cell
 CC adhesion molecule E-selectin was also examined. The present sequence is
 CC human JNK2 DNA. This sequence was used to generate the JNK2 antisense
 CC oligonucleotide. The antisense oligonucleotides used in the method
 CC contained modifications, namely phosphorothioate linkages and
 CC 2-methoxyethoxy bases. Some C residues also had a 5'methyl modification.
 CC Inhibitors of the TNF alpha signalling molecules have antibacterial,
 CC immunosuppressive, antipsoriatic, antidiabetic, antithyroid, cytostatic,
 CC dermatological, antiallergic and antiinflammatory activity. The antisense
 CC inhibitors may be useful for the treatment of sepsis, rheumatoid
 CC arthritis, inflammatory, immune disease, inflammatory bowel disease,
 CC allergic contact dermatitis, psoriasis, diabetes, Grave's disease,
 CC allograft rejection and cancer

XX SQ Sequence 1782 BP; 541 A; 359 C; 404 G; 478 T; 0 U; 0 Other;
 Query Match 6.0%; Score 48.4; DB 3; Length 1782;
 Best Local Similarity 74.4%; Pred. No. 0.41; 21; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 21

QY 630 CTGAAGAGAGGCTGCTTTTACTACACATTTTGTCTTCTTGAATTCATTA 689
 DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACATCTTGTCTTCTTCCCAATCCATGA 1137
 QY 690 CTTCCTTGATAGATAGTCTGT 711
 DB 1136 CTTCCTTGATAGATAGTCTGT 1115

Search completed: July 19, 2006, 18:53:02
 Job time : 658 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:42:15 ; Search time 4914 Seconds
(without alignments)
9103.676 Million cell updates/sec

Title: US10723681MOD.SEQ
Perfect score: 800
Sequence: 1 acatttcctcaactctta.....caataatcgttcgacg 800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
EST.*
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the chance being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	397.8	49.7	401 11	AQ046186	AQ046186 RBC11-11
C 2	293.2	36.6	393 11	AQ129390	AQ129390 HS 3045_A
C 3	82.8	10.3	247 2	BG204609	BG204609 RST24016
C 4	82.8	10.3	330 4	CB069799	CB069799 182907.Y
C 5	82.8	10.3	407 2	BF856752	BF856752 QV1-FT020
C 6	82.8	10.3	429 7	AM297251	AM297251 UI-H-BW0
C 7	82.8	10.3	448 1	AA663771	AA663771 aeg6h10.8
C 8	82.8	10.3	512 3	BM704479	BM704479 UI-B-CK1-
C 9	82.8	10.3	595 5	BM508552	BM508552 1137411.Y
C 10	82.8	10.3	605 5	CK825957	CK825957 1136103.Y
C 11	82.8	10.3	618 3	BQ287873	BQ287873 1K36103.X
C 12	82.8	10.3	921 10	DR762335	DR762335 HESCA 139
C 13	82.8	10.3	933 2	BI824308	BI824308 603040725
C 14	81.8	10.2	462 4	BX282592	BX282592 BX282592
C 15	80.4	10.1	315 2	BG219861	BG219861 RST39628
C 16	80.4	10.1	386 2	BF858136	BF858136 QV1-FT020
C 17	80.4	10.1	457 4	CB069160	CB069160 1613901.X
C 18	80.4	10.1	789 2	BG194386	BG194386 RST15333
C 19	78.8	9.8	257 2	BG209408	BG209408 RST28923

C 20	78	9.8	836	5	CJ443965	CJ443965
C 21	77.2	9.7	263	5	CR859197	CR859197 Pongo Pyg
C 22	76.4	9.6	296	5	CF408692	CF408692 CH3H05E_B
C 23	75.6	9.4	818	5	CJ491725	CJ491725
C 24	75.4	9.4	568	9	DA807178	DA807178
C 25	73.2	9.2	408	2	BF857793	BF857793 QV1-FT020
C 26	70	8.8	423	7	AM314598	AM314598 10855 MAR
C 27	70	8.8	708	9	DN543033	DN543033 1391834 M
C 28	69.6	8.7	390	7	BE72856	BE72856 205445 MA
C 29	69.6	8.7	351	7	BE72856	BE72856 205425 MA
C 30	69	8.6	916	10	DV915213	DV915213 LB0288.CR
C 31	68.8	8.6	332	4	BE126616	BE126616 BY126616
C 32	68.4	8.6	543	7	BE652295	BE652295 UI-M-AH0-
C 33	68.4	8.6	543	7	BE652295	BE652295 UI-M-AH0-
C 34	68.4	8.6	543	7	BE652295	BE652295 UI-M-AH0-
C 35	68.4	8.6	543	7	BE652295	BE652295 UI-M-AH0-
C 36	68.4	8.6	543	7	BE652295	BE652295 UI-M-AH0-
C 37	68.4	8.6	543	7	BE652295	BE652295 UI-M-AH0-
C 38	67.8	8.5	561	2	BF854904	BF854904 MRI-FN021
C 39	67	8.4	2629	6	AK163206	AK163206 Mus muscu
C 40	66.8	8.3	576	4	CB607972	CB607972 ANGNUNC:N
C 41	66	8.2	570	5	CF535846	CF535846 UI-M-GH0-
C 42	66	8.2	578	3	BM944347	BM944347 UI-M-EH0P
C 43	66	8.2	639	8	CX221469	CX221469 MNS38129
C 44	66	8.2	721	5	CF951683	CF951683 UI-M-HL0-
C 45	66	8.2	740	3	BM943588	BM943588 UI-M-EM0-
C 46	66	8.2	802	9	CX852086	CX852086 JGI CAAL8
C 47	64.4	8.1	642	3	BP485311	BP485311 BP485311
C 48	64	8.0	331	3	BU389929	BU389929 603804227
C 49	59	7.4	778	2	BJ725204	BJ725204 BJ725204
C 50	55.8	7.0	645	8	CX143962	CX143962 1283656 N
C 51	55.8	7.0	646	8	CX143963	CX143963 1283657 N
C 52	55.8	7.0	733	10	DT23168	DT23168 JGI CAAT7
C 53	54	6.8	733	5	CK638880	CK638880 UI-M-HO0-
C 54	54	6.8	825	1	AF064929	AF064929 AF064929
C 55	54	6.8	1284	14	AY411698	AY411698 Mus muscu
C 56	54	6.8	2590	6	AK139498	AK139498 Mus muscu
C 57	53.2	6.7	1060	14	CNS0047R	CNS0047R
C 58	52.8	6.6	425	2	BJ720556	BJ720556
C 59	51.8	6.5	801	14	BX142194	BX142194 Dario rer
C 60	51.6	6.5	500	5	CD803749	CD803749 UI-M-GV0-
C 61	51.6	6.5	652	4	CA324408	CA324408 UI-M-FY0-
C 62	51.6	6.5	654	7	BB253136	BB253136 BB253136
C 63	51.6	6.5	1466	6	AK043102	AK043102 Mus muscu
C 64	51	6.4	948	14	CNS0171M	CNS0171M
C 65	50.8	6.3	697	4	CA057984	CA057984 Bsalrgb54
C 66	50.8	6.3	708	7	AW914916	AW914916 EST346220
C 67	50.8	6.3	928	14	CNS000DKY	AL071865 Drosophill
C 68	50.8	6.3	1167	14	CNS07360	AL427102 Clome BAO
C 69	50	6.2	763	2	BM414648	BM414648 ECC00114
C 70	50	6.2	784	5	CK637229	CK637229 UI-M-HO0-
C 71	50	6.2	801	2	BI820604	BI820604 603034845
C 72	49.8	6.2	987	14	CNS014PQ	AL104456 Drosophill
C 73	49.8	6.2	1092	14	CNS020X7	AL104456 Drosophill
C 74	49	6.1	1101	14	CNS0039G	AL063921 Drosophill
C 75	48.8	6.1	928	14	CNS00DKY	AL071865 Drosophill
C 76	48.4	6.0	324	1	AA251966	AA251966 2811409 r
C 77	48.4	6.0	458	3	BM689515	BM689515 UI-E-CK1-
C 78	48.4	6.0	465	3	BQ187463	BQ187463 UI-E-CK1-
C 79	48.4	6.0	496	10	H1067	H1067 ym20b12.r1
C 80	48.4	6.0	516	4	BX282296	BX282296
C 81	48.4	6.0	565	9	DA405535	DA405535 DA405535
C 82	48.4	6.0	571	9	DA195866	DA195866 DA195866
C 83	48.4	6.0	572	3	BQ185526	BQ185526 UI-E-EJ1-
C 84	48.4	6.0	592	7	AW502260	AW502260 UI-HF-BNO
C 85	48.4	6.0	686	14	CR914758	CR914758 Sub sciof
C 86	48.4	6.0	697	7	CF787382	CF787382 855274 MA
C 87	48.4	6.0	704	8	CN145573	CN145573 994927 MA
C 88	48.4	6.0	714	1	AL119951	AL119951 DKFZ761C
C 89	48.4	6.0	754	3	CR549979	CR549979 DKFZP59B
C 90	48.4	6.0	759	3	B0852625	B0852625 ACENECOURT
C 91	48.4	6.0	764	14	CT237644	CT237644 Sub sciof
C 92	48.4	6.0	942	1	AL539761	AL539761

```
c 93 48.4 6.0 1033 1 AJ927386
c 94 48.4 6.0 1101 14 CNS00007
c 95 48.4 6.0 1118 4 BX403747
c 96 47.8 6.0 754 1 AQ951683
c 97 47.6 6.0 512 14 CR339134
c 98 47.6 6.0 660 14 CR466489
c 99 47.6 6.0 897 12 CG933873
c 100 47.4 5.9 251 1 AA333513
```

ALIGNMENTS

```
RESULT 1
LOCUS A0046186/c 401 bp DNA linear GSS 14-Apr-1999
DEFINITION Rpci11-31H10.TV Rpci-11 Homo sapiens genomic clone Rpci-11-31H10,
ACCESSION A0046186
VERSION A0046186.1 GI:3315113
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 401)
Adams,M.D., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1998)

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadam@igf.org

Clones are derived from the human BAC library Rpci-11. For BAC

library availability, please contact Pieter de Jong

(pieterdejong.med.bu@iag.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.bu@iag.edu/ordering>) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.cigr.org/ctdb/humgen/bac_end_search/bac_end_search.html

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..401

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="GDB:7511697"

/db_xref="taxon:9606"

/clone="Rpci-11-31H10"

/sex="Male"

/cell_type="Lymphocytes"

/clone_lib="Rpci-11"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

Rpci11 Human Male BAC Library"

ORIGIN

Query Match 49.7%; Score 397.8; DB 11; Length 401;

Best Local Similarity 99.5%; Pred. No. 1.2e-80;

Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 280 AGATTACTGAGCTCCACATTTGACTGATGCTCAAAAGGCAATTAGCTGCAATTTTG 339

DB 401 AGATTACTGAGCTCCACATTTGACTGATGCTCAAAAGGCAATTAGCTGCAATTTTG 342

QY 340 ATGAGGACATTTACCTTTAGCCCATGTTAAACATTTCTTTCGAGATTCATTTCTA 399

DB 341 ATGAGGACATTTACCTTTAGCCCATGTTAAACATTTCTTTCGAGATTCATTTCTA 282

QY 400 AATTATTATGAAAGTTTGTCTGATCATTTACATCAGATTAATGATGATGATG 459

```
Db 281 AATTATTATGAAAGTTTGTCTGATCATTTACATCAGATTAATGATGATG 222
QY 460 CCACACTGATATTCAAAGAAATTTAAATCATTTATAGACACACATGATGATA 519
Db 221 CCACACTGATATTCAAAGAAATTTAAATCATTTATAGACACACATGATGATA 162
QY 520 TTGTGTCATCTGCTCTTTTAAAGCAATGTTATTTCTTTCGACACCCCTACAAAGGCC 579
Db 161 TTGTGTCATCTGCTCTTTTAAAGCAATGTTATTTCTTTCGACACCCCTACAAAGGCC 102
QY 580 AAGAAATTACACAGACTAGTTATTTGTTATTCACGAGAGTACTGAGAGAGA 639
Db 101 AAGAAATTACACAGACTAGTTATTTGTTATTCACGAGAGTACTGAGAGAGA 42
QY 640 AGGCTGCTCTTTTACTACACCAATTTTACTCTTTCTCTG 680
Db 41 AGGCTGCTCTTTTACTACACCAATTTTACTCTTTCTCTG 1
```

RESULT 2

LOCUS A0129390/c 393 bp DNA linear GSS 23-SEP-1998

DEFINITION HS 3045 A2 F04 MR CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=3045 Col=8 Row=K, genomic survey

sequence.

ACCESSION A0129390

VERSION A0129390.1 GI:3506556

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 393)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 3045 Row: K Column: 8

Class: BAC ends

High quality sequence stop: 393.

FEATURES

source

Location/Qualifiers

1..393

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=3045 Col=8 Row=K"

/sex="male"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in

E-Coli DH10B"

ORIGIN

Query Match 36.6%; Score 293.2; DB 11; Length 393;

Best Local Similarity 91.7%; Pred. No. 1.3e-56;

Matches 321; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 331 TGAATTTGATGAGGACATTT-TACCCTTTCAGCCCATGTTATCATTTCTTTCAGATTTCA 389

Db 330 TCAATTTGATGAGGACATTTTCATTTAGGACATGTTACATTTGTTTCAGATTTCA 291


```

QY 390 TTACTATTAATTAATTAAGATTTTTCCTGATCATTAACATCAGATATC 449
DB 290 TTACTATTAAGTATATATTAAGTTTCTGATGATCATTCATTCAGATATC 231
QY 450 AGAATGATGCACTGATATATCAAAAGAAATAAATCAATATTAAGACACAA 509
DB 230 AGAATGATGCAATGATATCAAGAAATGAACTAAAGTCATTAAGACACAA 171
QY 510 CCATGATATTTTTCATCTGCTCTTTAAGCAATGTTATGTTTTCGAAACCCCTA 569
DB 170 CCATGATATTTTTCATCTGCTCTTTAAGCAATGTTATGTTTTCGAAACCCCTA 111
QY 570 CACAAGGCAAGAAATTAACAAGTACTGTTATGTTATGATCAGGAGAGATAC 629
DB 110 CACAAGGCAAGAAATTAACAAGTACTGTTATGTTATGATCAGGAGAGATAC 51
QY 630 CTGAGAGAGAGGCTGCTTTTCTACTACACATTTTACTTTCTTCT 679
DB 50 CTGAGAGAGAGGCTGCTTTTCTACTACACATTTTACTTTCTTCT 1

RESULT 3
BC204609/c 247 bp mRNA linear EST 21-Apr-2001
LOCUS RST24016 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BC204609
VERSION BC204609.1 GI:13726296
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 247)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Kika, A., Hess, J., Cochren, K., Lo, K.,
Offendack, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
JOURNAL PUBMED
COMMENT Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atherys.com
High quality sequence stop: 197.
Location/Qualifiers
source
1. .247
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Atherys RAGE Library"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 247;
Best Local Similarity 97.7%; Pred. No. 2.8e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTTTTACTACACATTTTACTTTCTTCTGAATC 685
DB 150 GCACCTGAAGAGAGGCTGCTTTTACTACACATTTTACTTTCTTCTGAATC 91

```

```

QY 686 ATTACTCTCTTGAGTAACTCTGT 711
DB 90 ATTACTCTCTTGAGTAACTCTTT 65

RESULT 4
CB069799/c 390 bp mRNA linear EST 21-JUN-2003
LOCUS 1829507.y1 HR85 islet Homo sapiens cDNA clone IMAGE:653861 5
DEFINITION similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
; mRNA sequence.
ACCESSION CB069799
VERSION CB069799.1 GI:27814319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 390)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Maira, M., Page, D., Wylie, T., Martin, J., Bistain, A.,
Schmitt, A., Treising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1829507.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 345.
Location/Qualifiers
source
1. .390
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:653861"
/cisue_type="Purified pancreatic islet"
/clone_lib="HR85 islet"
/lab_host="DH10B"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-562-1916, Fax: 314-747-2692."

ORIGIN
Query Match 10.3%; Score 82.8; DB 4; Length 390;
Best Local Similarity 97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTTTTACTACACATTTTGTCTTCTGTAATC 685
DB 138 GCACCTGAAGAGAGGCTGCTTTTACTACACATTTTGTCTTCTGTAATC 79
QY 686 ATTACTCTCTTGAGTAACTCTGT 711

```

Db 78 ATTACTCTGTGATGATGATCTTT 53

RESULT 5
BF856752/c 407 bp mRNA linear EST 16-JAN-2001
LOCUS QV1-F10202-021100-455-f02 F10202 Homo sapiens cDNA, mRNA sequence.
DEFINITION
VERSION BF856752 GI:12244496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 407)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W.J.F., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml.pl?file=QV1-F10202-021100-455-f02&ct=2000-11-02&ct=41)
Seq primer: puc 18 forward
High quality sequence stop: 407.
Location/Qualifiers
1. 407
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0202"
/note="Organ: prostate tumor; Vector: puc18; Site: 1; Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Query Match 10.3%; Score 82.8; DB 2; Length 407;
Best Local Similarity 97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTCACGAGGAGGAGGCTCTTTTACACACATTTTACTCTTTCTTGAAATTC 685
DB 99 GCACCGAGGAGGAGGCTCTCTTTTACACACATTTTACTCTTTCTTGAAATTC 40
QY 686 ATTACTCTGTGATGATGATCTTT 711
DB 39 ATTACTCTGTGATGATGATCTTT 14

RESULT 6
AM297251/c 429 bp mRNA linear EST 16-JAN-2000
LOCUS UI-H-BW0-aj1-b-12-0-UI.61 NCI_CGAP_Sub6 Homo sapiens cDNA clone
DEFINITION

IMAGE:2731750 3', mRNA sequence.
AM297251
VERSION AM297251.1 GI:6703887
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 429)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
JOURNAL
PUBMED
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www.bio.illnl.gov/biryp/image.html
Seq primer: M13 Forward
POLY(A)=yes.
Location/Qualifiers
1. 429
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2731750"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub6"
/note="Vector: pT7T3D-Pac1; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub6 is a subcloned library derived from BW, which consists of a mixture of four normalized libraries: NCI CGAP Brn50, NCI CGAP Lu13, NCI CGAP Ovis, GBC1. The NCI CGAP Sub6 library had 7 million recombinants. A single-stranded DNA preparation of BW was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI CGAP Kid3 pool 1, LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456775, 1500552-1500855); NCI CGAP Kid5 pool 1, LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831, 1471368-1472903, 1492104-1493253); NCI CGAP Lu5 pool 1, LLAM 3575-3582, 3651-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1, LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 147592-1476743); NCI CGAP Pr22 pool 1, LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Colo pool 1, LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351). (50% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clonoids 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-2712455) and (20% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2723591) (30% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_LIB=NCI CGAP-Lu13
TAG_SEQ=GCGCG"
ORIGIN
Query Match 10.3%; Score 82.8; DB 7; Length 429;
Best Local Similarity 97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTCACGAGGAGGAGGCTCTTTTACACACATTTTACTCTTTCTTGAAATTC 685

```

Db      291 GCACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAACTTTCTTCGAAATTC 232
Qy      686 ATTACTCTCTGTGATAGATTCTGT 711
Db      231 ATTACTCTCTGTGATAGATTCTTT 206

RESULT 7
LOCUS   AA663771
DEFINITION ae68h10.s1 StrataGene schizo brain S11 Homo sapiens cDNA clone
IMAGE:969379 3' similar to SW:JNK3 RAT P49187 STRESS-ACTIVATED
PROTEIN KINASE JNK3 ; , mRNA sequence.
ACCESSION AA663771
VERSION   AA663771.1 GI:2617762
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 448)
AUTHORS  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Stepcevic,M., Tan,F.,
Theisinger,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
JOURNAL  WashU-NCI human EST Project
COMMENT   Unpublished (1997)
          Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@wustl.wustl.edu
          This clone is available royalty-free through LMLT; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Possible reversed clone: similarity on wrong strand
          Seq primer: -40m13 fwd. ET from Amersham
          High quality sequence stop: 350.
          Location/Qualifiers
            1..448
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:969379"
               /sex="male"
               /tissue_type="schizophrenic brain S-11 frontal lobe"
               /dev_stage="34 years old"
               /lab_host="SOLR (kanamycin resistant)"
               /clone_id="StrataGene schizo brain S11"
               /note="Vector: Bluescript SK-; Site 1: EcoRI; Library
               constructed from S-11 frontal lobe, male, 34 years old,
               50% caucasian, 50% Aleutian. Schizophrenic suicide.
               Random primed into EcoRI site of ZAP II Vector. Mass
               excised. Custom library. Avg insert length 1.4kb.
               Material obtained by Johnston N., Torrey, E.F., Yolken R.,
               and the Stanley Neuropathology Consortium - Analysis of
               RNAs from the Brains of Individuals with Psychiatric
               Diseases (Unpublished) Stanley Neuropathology Laboratory,
               Johns Hopkins School of Medicine, Baltimore MD."

ORIGIN
Query Match      10.3%; Score 82.8; DB 1; Length 448;
Best Local Similarity . 97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      626 GTACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAACTTTCTTCGAAATTC 685
Db      210 GCACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAACTTTCTTCGAAATTC 269
Qy      686 ATTACTCTCTGTGATAGATTCTGT 711

```

```

Db      270 ATTACTCTCTGTGATAGATTCTTT 295

RESULT 8
LOCUS   BM704479/c
DEFINITION UI-E-CK1-agb-1-15-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone
IMAGE:969379 3' similar to SW:JNK3 RAT P49187 STRESS-ACTIVATED
PROTEIN KINASE JNK3 ; , mRNA sequence.
ACCESSION BM704479
VERSION   BM704479.1 GI:19017737
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 512)
AUTHORS  Bonaldo,M.F., Lennon,G. and Soares,M.B.
JOURNAL  Normalization and subtraction: two approaches to facilitate gene
COMMENT   discovery
          Genome Res. 6 (9), 791-806 (1996)
          8889548
          Contact: Soares, MB
          Coordinated Laboratory for Computational Genomics
          University of Iowa
          375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: bento-soares@uiowa.edu
          Tissue Procurement: Dr. Gregg Hageman
          CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Researchers may obtain clones from Research
          Genetics (www.resgen.com).
          Seq primer: M13 Reverse.
          Location/Qualifiers
            1..512
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="UI-E-CK1-agb-1-15-0-UI"
               /tissue_type="Retina Foveal and Macular"
               /dev_stage="adult"
               /lab_host="DH10B (life Technologies) (T1 phage resistant)"
               /clone_id="UI-E-CK1"
               /note="Organ: eye; Vector: pRT73-Pac (Pharmacia) with a
               modified polylinker; Site 1: EcoR I; Site 2: Not I;
               UI-E-CK1 is a normalized cDNA library containing the
               following tissue(s): Retina Foveal and Macular. The
               library was constructed according to Bonaldo, Lennon and
               Soares, Genome Research, 6:791-806, 1996. First strand
               cDNA synthesis was primed with an oligo-dT primer
               containing a Not I site. Double stranded cDNA was ligated
               to an EcoR I adaptor, digested with Not I, and cloned
               directionally into pRT73-Pac vector. The oligonucleotide
               used to prime the synthesis of first-strand cDNA contains
               a library tag sequence that is located between the Not I
               site and the (dT)18 tail. The sequence tag for this
               library is GACC. This library was created for the program,
               Gene Discovery in the Visual System, supported by National
               Eye Institute (NEI)."

ORIGIN
Query Match      10.3%; Score 82.8; DB 3; Length 512;
Best Local Similarity . 97.7%; Pred. No. 2.9e-08;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      626 GTACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAACTTTCTTCGAAATTC 685
Db      413 GCACCTGAAGAGAGGCTGTCCTTTACTACACCATTTTAACTTTCTTCGAAATTC 354

```

Oy 686 ATTACTTCCTGTGATAGATTCTGT 711
 Db 353 ATTACTTCCTGTGATAGATTCTTT 328

RESULT 9
 BM508552/c
 LOCUS
 DEFINITION BM508552 595 bp mRNA linear EST 12-MAR-2002
 1137A11.Y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
 musculus cDNA IMAGE:5943836 5' similar to SW:MK10_HUMAN
 P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10 ; mRNA sequence.
 BM508552
 VERSION BM508552.1 GI:18679695
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murine; Mus.

REFERENCE
 AUTHORS Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, D., Blistein, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: 1137A11.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Harvard University, Howard Hughes Medical Institute
 Endocrine Pancreas Consortium
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu)
 MGI:2006708 This sequence now available from the IMAGE consortium,
 for clone orders contact: info@image.llnl.gov
 Seg primer: -40RP from Gibco
 High quality sequence stop: 430.
 Location/Qualifiers

FEATURES
 source
 1..595
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="ICR"
 /db_xref="taxon:10090"
 /clone="IMAGE:5943836"
 /sex="Both for embryonic & newborn, male for adult and
 adult islet"
 /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
 adult, mixed"
 /lab_host="DH10B"
 /clone_id="Melton Normalized Mixed Mouse Pancreas 1
 N1-MMS1"
 /note="Vector: DSPORT1, Site 1: Not I; Site 2: Sal I; Five
 libraries representing E10.5/12.5 pancreatic bud, E12.5
 pancreas, newborn pancreas, adult pancreas, and adult
 islets of Langerhans were separately constructed using
 Superscript Plasmid Library Kit (Life Technologies). cDNA
 was made by oligo-dT priming and size-selected by column
 fractionation. Libraries were amplified once on solid
 support and plasmid DNA from each library was prepared
 and mixed in equal amounts. The mixed library DNA was
 normalized by method #4 from Bionardo, Lennon, and Soares
 1996 Genome Research 6:791-806; 0.5 microgram
 single-stranded mixed library plasmid DNA was mixed with
 5 micrograms PCR product representing mixed library
 inserts and hybridized to an EcoT of 6. Single-stranded

ORIGIN
 Query Match 10.3%; Score 82.8; DB 2; Length 595;
 Best Local Similarity 97.7%; Pred. No. 3e-08;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 626 GTACTGAGAGAGAGAGCTGCTCTTTACTACACATTTTACTGCTTTCTTGAATTC 685
 Db 471 GCACCTGAGAGAGAGAGCTGCTCTTTACTACACATTTTACTGCTTTCTTGAATTC 412

Oy 686 ATTACTTCCTGTGATAGATTCTGT 711
 Db 411 ATTACTTCCTGTGATAGATTCTTT 386

RESULT 10
 CK825957
 LOCUS
 DEFINITION CK825957 605 bp mRNA linear EST 11-MAR-2004
 1K36F03.Y5 HR85 islet Homo sapiens cDNA clone IMAGE:5783165 5'
 similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
 ; mRNA sequence.
 CK825957
 VERSION CK825957.1 GI:44842882
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Cetrhini;
 Homidae; Homo.

REFERENCE
 AUTHORS Melton, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Pape, D.,
 Wylie, T., Martin, J., Blistein, A., Schmitt, A., Theising, B.,
 Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M.,
 McCann, R., Cole, R., Tsagaris, R., Williams, T., Jackson, Y. and
 Bowers, Y.
 Washu-Harvard Pancreas EST Project
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 This read is a 5' RESEQUENCE of a previously sequenced pancreas
 clone
 Good hit to opposite strand read. . . wrong orientation BUT PASSED FOR
 MOUSE-PANCREAS VERIFICATION
 Possible reversed clone: similarity on wrong strand
 Seg primer: -40UP from Gibco
 High quality sequence stop: 570.
 Location/Qualifiers

FEATURES
 source
 1..605
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5783165"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_id="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size
 3.5 kb. Site was destroyed after directional cloning.
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 10.3%; Score 82.8; DB 5; Length 605;
 Best Local Similarity 97.7%; Pred. No. 3e-08;
 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGCTGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
 DB 323 GCACCTGAAGAGAGAGCTGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 382
 QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
 DB 383 ATTACTCTCTGTAGATAGTTCTTT 408

RESULT 11
 LOCUS BQ287873 618 bp mRNA linear EST 14-MAY-2002
 DEFINITION 136103.X1 HR85 islet Homo sapiens cDNA clone IMAGE:5783165 3',
 similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10
 ;, mRNA sequence.

ACCESSION BQ287873.1 GI:20658904
 VERSION BQ287873
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo
 1 (bases 1 to 618)
 TITLE Melton, D., Brown, J., Keny, G., Permut, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., R.,
 Williams, T., Jackson, Y., and Bowers, J.
 JOURNAL Endocrine Pancreas Consortium
 COMMENT Unpublished (2000)
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@iobp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 369.
 Location/Qualifiers

FEATURES

source

1. 618
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5783165"
 /cissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
 NotI; Site_2: XhoI; cDNA made by oligo-dT priming
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permut Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 10.3%; Score 82.8; DB 3; Length 618;
 Best Local Similarity 97.7%; Pred. No. 3e-08;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 626 GTACCTGAAGAGAGAGCTGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
 DB 312 GCACCTGAAGAGAGAGCTGTCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 371
 QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
 DB 372 ATTACTCTCTGTAGATAGTTCTTT 397

RESULT 12
 LOCUS DR762335/c 921 bp mRNA linear EST 21-JUL-2005
 DEFINITION HESC4_139_B07_g1_A037 NIH_MGC_262 Homo sapiens cDNA clone
 IMAGE:7971903 5', mRNA sequence.
 ACCESSION DR762335
 VERSION DR762335
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgsbds-remail.nih.gov

Tissue Procurement: BresaGen, Inc.
 cDNA Library Preparation: Express Genomics, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
 University of Georgia
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.llnl.gov
 plate: L1AM 17089 row: d column: 13
 Seq primer: JENREV (CAGGAACAGCATGACC)
 High quality sequence stop: 921.
 Location/Qualifiers

FEATURES

source

1. 921
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7971903"
 /sex="male"
 /cissue_type="embryonic stem"
 /cell_type="human embryonic stem cells"
 /cell_line="BG01"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_1ib="NIH_MGC_262"
 /note="Vector: pEXpress-1; Site_1: NotI; Site_2: EcoRV;
 RNA obtained from human embryonic stem cells isolated from
 the inner cell mass of blastocyst stage embryos and
 differentiated to an early neural progenitor cell type.
 Cell line id and NIH Registry designation is BG01.
 Positive for Nestin and Musashi expression. Passage number
 18. cDNA primed using oligo-dT primer:
 5'-pACTAGTTCATGATCGCAGCGCGCCGCTT25-3' and cloned into
 the EcoRV/NotI sites of pEXpress-1. This primary library
 is non-normalized (normalized primary library is
 NIH MGC 259). It was constructed by Express Genomics
 (Frederick, MD). Sequence ends have been trimmed to
 exclude vector and regions below phred quality 16. Note:
 this is a Mammalian Gene Collection library."

ORIGIN

Query Match 10.3%; Score 82.8; DB 10; Length 921;
 Best Local Similarity 97.7%; Pred. No. 3e-08;

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 315)
Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Booser, S., Whittington, J., Letner, L., Costanzo, D., McEligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kika, A., Hess, J., Cochren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 265.
Location/Qualifiers
1. .315
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 315;
Best Local Similarity 98.8%; Pred. No. 1e-07; 1; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
DB 142 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 83
QY 690 CTTCCTTGTAGATAGTTCGT 711
DB 82 CTTCCTTGTAGATAGTTCGT 61

RESULT 16
BF858136 386 bp mRNA linear EST 16-JAN-2001
LOCUS BF858136
DEFINITION QV1-PT0202-131100-470-c12 PT0202 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858136
VERSION BF858136.1 GI:12245880
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 386)
Dias, Neco, E., Garcia, Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. P., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brenhan, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
10737800
CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FADESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1c2=QV1-PT0202-131100-470-c12&tl=2000-11-13&tl=1)
Seq primer: puc 18 forward
High quality sequence stop: 386.
Location/Qualifiers
1. .386
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="PT0202"
/note="Organ: prostate tumor; Vector: puc18; Site: 1; SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 10.1%; Score 80.4; DB 2; Length 386;
Best Local Similarity 98.8%; Pred. No. 1e-07; 1; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 689
DB 114 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTGAATTCATTA 55
QY 690 CTTCCTTGTAGATAGTTCGT 711
DB 54 CTTCCTTGTAGATAGTTCGT 33

RESULT 17
CB069160 457 bp mRNA linear EST 21-JAN-2003
LOCUS CB069160
DEFINITION ts13901.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6364968 3' similar to SM:MK10_HUMAN P53779 MITOGEN-ACTIVATED PROTEIN KINASE 10 ; mRNA sequence.
ACCESSION CB069160
VERSION CB069160.1 GI:27813680
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 457)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K., Lemishka, I., Scaese, M., Bresnelli, J. J., Gradwohl, G., Clifton, S., Hillier, L., Merritt, M., Pape, D., Wylie, T., Martin, J., Blais, A., Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, V., Williams, T., Jackson, Y. and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gldco
 High quality sequence stop: 369.
 Location/Qualifiers
 1..457
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="6364958"
 /cissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); site_1:
 NotI; site_2: XhoI; cDNA made by oligo-dT priming.
 Size selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permut Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 10.1%; Score 80.4; DB 4; Length 457;
 Best Local Similarity 98.8%; Pred. No. 1e-07;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGCGTCTCTTTTACTACACCAATTTTCTTTCTTGAATTCATTA 669
 DB 313 CTGAGAGAGAGCGTCTCTTTTACTACACCAATTTTCTTTCTTGAATTCATTA 372
 QY 690 CTTCCTGTGATTAAGTTCTGT 711
 DB 373 CTTCCTGTGATTAAGTTCTTT 394

RESULT 18
 BG194386/c 789 bp mRNA linear EST 21-APR-2001
 LOCUS RST13533 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG194386
 ACCESSION BG194386.1 GI:13716073
 VERSION BG194386.1 GI:13716073
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 789)
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
 Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozar,S.,
 Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
 Offenbacher,J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 JOURNAL 11329013
 PUBMED
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 397.
 Location/Qualifiers
 1..789
 /organism="Homo sapiens"

FEATURES
 source

ORIGIN

Query Match 10.1%; Score 80.4; DB 2; Length 789;
 Best Local Similarity 98.8%; Pred. No. 1.1e-07;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGCGTCTCTTTTACTACACCAATTTTCTTTCTTGAATTCATTA 689
 DB 142 CTGAGAGAGAGCGTCTCTTTTACTACACCAATTTTCTTTCTTGAATTCATTA 83
 QY 690 CTTCCTGTGATTAAGTTCTGT 711
 DB 82 CTTCCTGTGATTAAGTTCTTT 61

RESULT 19
 BG209408/c 257 bp mRNA linear EST 21-APR-2001
 LOCUS RST28923 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG209408
 ACCESSION BG209408
 VERSION BG209408.1 GI:13731095
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo (257)
 1 (bases 1 to 257)
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
 Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozar,S.,
 Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
 Offenbacher,J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 JOURNAL 11329013
 PUBMED
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 207.
 Location/Qualifiers
 1..257
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 9.8%; Score 78.8; DB 2; Length 257;
 Best Local Similarity 97.6%; Pred. No. 2.3e-07;
 Matches 80; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATCATTA 689
 |||||
 Db 147 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATCATTA 88
 |||||
 Oy 690 CTTCCTTGTAGATTAAGTTCTGT 711
 |||||
 Db 87 CTTCCTTGTAGATTAAGTTCTTT 66
 |||||

RESULT 20
 Cj443965/c 836 bp mRNA linear EST 06-OCT-2005

LOCUS Cj443965 macaque brain cDNA library QcCE Macaca fascicularis cDNA
 DEFINITION clone QcCE-21545 5', mRNA sequence.

ACCESSION Cj443965
 VERSION Cj443965.1 GI:77250642
 KEYWORDS EST.
 SOURCE Macaca fascicularis (craab-eating macaque)
 ORGANISM Macaca fascicularis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecidae; Cercopithecinae; Macaca.

AUTHORS 1 (bases 1 to 836)
 Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirata, M., Terao, K.,
 Suzuki, Y., Sugano, S. and Hashimoto, K.
 TITLE Macaca fascicularis cDNA database
 JOURNAL Unpublished (2005)
 COMMENT Contact: Naoki Osada
 Division of Biomedical Resources
 National Institute of Biomedical Innovation
 Saito-Asagi 7-6-8, Ibaraki, Osaka, 567-0085, Japan
 Tel: 81-72-641-9811
 Fax: 81-72-641-9016
 Email: nosada@nibio.go.jp
 URL: http://genbank.nibio.go.jp/gbank/.

FEATURES
 source Location/Qualifiers

1. 836
 /organism="Macaca fascicularis"
 /mol_type="mRNA"
 /db_xref="taxon:9541"
 /clone="QcCE-21545"
 /sex="male"
 /tissue_type="cerebellum cortex"
 /dev_stage="adult"
 /lab_host="TOP10"
 /clone_lib="macaque brain cDNA library QcCE"
 /note="Vector: pME18-FL3 (Acc.No. AB009864); Site_1:
 DraIII (CACTGTGT); Site_2: DraIII (CACCATGTG); 1st strand
 cDNA was primed with an oligo(dT) primer
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was
 synthesized using specific 5' and 3' primers and amplified
 by PCR. The PCR product was digested with SfiI and size
 selection was performed to exclude fragments <1.5kb. The
 SfiI-digested PCR product was cloned into distinct DraIII
 sites of pME18-FL3. XhoI sites just outside the DraIII
 sites can be used to isolate the cDNA insert. Libraries
 were constructed by oligo-capping method."

ORIGIN

Query Match 9.8%; Score 78; DB 5; Length 836;
 Best Local Similarity 94.2%; Pred. No. 3.9e-07;
 Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 626 GTACCTTAAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTC 685
 |||||
 Db 122 GCACCTTAAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTC 63
 |||||
 Oy 686 ATTACTTCTTGTAGATTAAGTTCTGT 711
 |||||
 Db 62 ATTACTTCTTGTAGATTAAGTTCTTT 37
 |||||

RESULT 21

CR859197/c 2693 bp mRNA linear HTC 12-NOV-2004
 LOCUS CR859197
 DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp459H0638 (from clone DKFZp459H0638).
 ACCESSION CR859197
 VERSION CR859197.1 GI:55729296
 KEYWORDS HTC.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Pongo.
 1 (bases 1 to 2693)

AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
 Robo, G., Har, M. and Wiemann, S.
 TITLE The German cDNA Consortium
 JOURNAL Direct Submission
 Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuherberg, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the
 Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA
 sequencing consortium of the German Genome Project. This clone
 (DKFZp459H0638) is available at the RZPD Deutsches
 Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneID=DKFZp459H0638
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES
 source Location/Qualifiers

1. 2693
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp459H0638"
 /tissue_type="cortex"
 /clone_lib="459 (synonym: pcor1). Vector pSPORT1_SfiI; host
 DH10B; sites SfiI + SfiIb"
 /dev_stage="adult"
 /note="mitogen-activated protein kinase 10 isoform 3 (Homo
 sapiens), differentially spliced"
 1. 2693
 /gene="DKFZp459H0638"
 638. 1792
 /gene="DKFZp459H0638"
 /codon_start=1
 /product="hypothetical protein"
 /protein_id="CAH91384.1"
 /db_xref="GI:55729297"
 /translation="MSKSVNDQFVSVEVDSFTFLVLRVYONLKPISGAGNIVCAAY
 DAVLDNRVAIKLSRPFQHTAKARVRLVLMKCNHKNITSLNVPFQRTLEQFO
 DVLVVELMDANLCVITONELDHENRSLVLYVLCI KRLHSGIILHRDKPSNIVK
 SCKTKILDFGLARTAGTSFMMTPVYVTVRYVAPVILGMKENVYENRKYAGLTPKLEP
 VHKILFPERDYIDWNKVIIEQLGTPCEPFMKLOPTVANYENRKYAGLTPKLEP
 DSIYPADSDHNLKASQARDLSKMLVIDPARKISVDPLQHPYINWVDPAVEAEP
 PQIYBQDLDERHTIDEMKELIYKVMNSEKTKGNVAVGQSPSAQVQC"

ORIGIN

Query Match 9.7%; Score 77.2; DB 6; Length 2693;
 Best Local Similarity 96.3%; Pred. No. 6.5e-07;
 Matches 79; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 630 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 689
 |||||
 Db 1775 CTGAAGAGAGAGGCTGCTCTTTTACTACACCATTTTCTTTCTTCTGAAATTCATTA 1716
 |||||
 Oy 690 CTTCCTTGTAGATTAAGTTCTGT 711
 |||||
 Db 1715 CTTCCTTGTAGATTAAGTTCTTT 1694
 |||||

RESULT 22
 CF408692/c

```

REFERENCE      1 (bases 1 to 818)
AUTHORS        Osada,N., Hida,M., Kusuda,J., Tanuma,R., Hirata,M., Terao,K.,
TITLE          Suzuki,Y., Sugano,S. and Hashimoto,K.
JOURNAL        Macaca fascicularis cDNA database
COMMENT        Unpublished (2005)
                Contact: Naoki Osada
                Division of Biomedical Resources
                National Institute of Biomedical Innovation
                Saito-Aragi 7-6-8, Ibaraki, Osaka, 567-0085, Japan
                Tel: 81-72-641-9811
                Fax: 81-72-641-9016
                Email: nosada@nibio.go.jp
                URL: http://genebank.nibio.go.jp/gbank/.
FEATURES
  source
    1..818
       /organism="Macaca fascicularis"
       /mol_type="mRNA"
       /db_xref="taxon:9541"
       /clone="QcSA-19671"
       /sex="male"
       /issue_type="testis"
       /dev_stage="adult"
       /lab_host="QOP10"
       /clone_1lb="macaque testis cDNA library QcSA"
       /note="vector: pME185-FL3 (Acc.No. AB009864); Site_1:
       DraIII (CACTGTG); Site_2: DraIII (CACCATGTG); 1st strand
       cDNA was primed with an oligo(dT) primer
       (ATGAGCCCTTTTCTTTTCTTTTCTTTT); double-stranded cDNA was
       synthesized using specific 5' and 3' primers and amplified
       by PCR. The PCR product was digested with SfiI and size
       selection was performed to exclude fragments <1.5kb. The
       SfiI-digested PCR product was cloned into distinct DraIII
       sites of pME185-FL3. XhoI sites just outside the DraIII
       sites can be used to isolate the cDNA insert. Libraries
       were constructed by oligo-capping method."
ORIGIN
Query Match      9.4%; Score 75.6; DB 5; Length 818;
Best Local Similarity 95.1%; Prid. No. 1,4e-06;
Matches 78; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      630 CTGAGAGAGAGGCTGCTCCTTACTACACACCATTTTATGCTCTTCCTTGATTCATTA 689
        |||||
Db       611 CTGAGAGAGAGGCTGCTCCTTACTACACGCATTTTATGCTCTTCCTGCAATCATTA 552
        |||||

QY      690 CTTCCTTGATGATTAAGTTCTGT 711
        |||||
Db       551 CTTCCTTGATGATTAAGTTCTTT 530
        |||||

RESULT 24
DA807178/c      DA807178      568 bp      mRNA      linear      EST 11-NOV-2005
LOCUS          DA807178      OCEBBF3 Homo sapiens cDNA clone OCEBBF3022734 5', mRNA
DEFINITION    sequence.
ACCESSION    DA807178
VERSION      DA807178.1 GI:82045913
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homiidae; Homo.
  1 (bases 1 to 568)
    kumura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
    Yamashita,R., Yamamoto,C., Sekine,M., Tsutitani,K., Wakaguri,H.,
    Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
    Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuna,M.,
    Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
    Tanabe,T., Nagai,K., Kikuchi,H., Naka,K., Iseogi,T. and Sugano,S.
    Diversification of Transcriptional Modulation: Large-scale
    Identification and Characterization of Putative Alternative
    Promoters of Human Genes

```

JOURNAL
PUBMED
COMMENT

Genome Res. 16 (1), 55-65 (2006).
16344560
Contact: Takao Iwagaki
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdn@nifty.com
NEO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES
source

Location/Qualifiers
1..568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OCB8F3022734"
/issue_type="Brain"
/dev_stage="fetal"
/clone_id="OCB8F3"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 9.4%; Score 75.4; DB 9; Length 568;
Best Local Similarity 98.7%; Pred. No. 1.5e-06;
Matches 76; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 635 GGAGAGGCTGCTCTTACTACACCAATTTAGCTTTCTTGATTCATCTCC 694
|||||
Db 568 GGAGAGGCTGCTCTTACTACACCAATTTAGCTTTCTTGATTCATCTCC 509
|||||

OY 695 TTGTAGATTAAGTTCTGT 711
|||||
Db 508 TTGTAGATTAAGTTCTTT 492
|||||

RESULT 25
BF857793

LOCUS BE857793 408 bp mRNA linear EST 16-JAN-2001
DEFINITION OY1-F70202-071100-465-a04 F70202 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF857793
VERSION BF857793.1 GI:12245537

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS 1 (bases 1 to 408)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bionas, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H.,
Bunster, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

FEATURES
source

(http://www.ludwig.org.br/scripts/gethtml2.pl?c1=QV1&c2=QV1-F70202-
071100-465-a04&c3=2000-11-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 325.
Location/Qualifiers
1..408

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="F70202"
/note="Organ: prostate tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 9.2%; Score 73.2; DB 2; Length 408;
Best Local Similarity 90.7%; Pred. No. 4.6e-06;
Matches 78; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 626 GTACCTGAGAGAGGCTGCTCTTACTACACCAATTTAGCTTTCTTGATTC 685
|||||
Db 308 GCACCTGAGAGAGGCTGCTCTTACTACACCAATTTAGCTTTCTTGATTC 367
|||||

OY 686 ATTACTTCTTGTAGATTAAGTTCTGT 711
|||||
Db 368 ATTACTTCTTGTAGATTAAGTTCTTT 393
|||||

RESULT 26
AW314598/c

LOCUS AW314598 423 bp mRNA linear EST 25-APR-2001
DEFINITION 10855 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW314598
VERSION AW314598.1 GI:6743854

KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM

REFERENCE
AUTHORS Smith, T.F.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrnenkung, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perera, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

FOR PRIMERS AGGAACACGATGACCAT
BACKWARD: GTTTCACGACGACG
Plate: 9 row: D column: 1
Seq primer: ATTAGTGACACTAG.

FEATURES
source

1..423
/organism="Bos taurus"
/mol_type="mRNA"

KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 551)
Smith, T.P.L., Groves, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Beumelt, G.L., Heaton, M.P., Laegreid, W.W., Kohrer, G.A., Chitko-Mckown, C.G., Perte, G., Holt, I., Karaycheva, S., Liang, F., Quackenbush, J., and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE
JOURNAL
PUBMED 11282978

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smt@meat1.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 46 row: M column: 8
Seq primer: ATTACGTCACATATAG.
Location/Qualifiers
1. .551
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2B0V"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

ORIGIN
Query Match 8.7%; Score 69.6; DB 7; Length 551;
Best Local Similarity 89.3%; Pred. No. 3.2e-05;
Matches 75; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGGAATTC 685
DB 85 GCACCTGAAGAGAGGCTGTCTTCTTCAACACCATTTCTTCTTCTCGAGTTC 26

QY 686 ATTACTCTCTTGATAGTATGTTCT 709
DB 25 ATTACTCTCTTATAGATGATTTCT 2

RESULT 30
DV915617/c 916 bp mRNA linear EST 01-DEC-2005
LOCUS LB0288.CR_F16 GC_BGC-28 Bos taurus cDNA clone IMAGE:8222610, mRNA
DEFINITION sequence.
DV915617
VERSION DV915617.1 GI:82971369
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 916)
Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shennan, C.,

TITLE
JOURNAL
COMMENT Contact: Robert Kirkpatrick
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia, Canada, V5Z 4S6
Tel: 1-604-707-5900 x5406
Fax: 1-604-876-3561
Email: robert.kirkpatrick@bc.ca
Insert Length: 916 Std Error: 0.00
Plate: LB0288 row: F column: 16
High quality sequence stop: 916.
Location/Qualifiers
1. .916
/organism="Bos taurus"
/mol_type="mRNA"
/strain="U1 Hereford"
/db_xref="taxon:9913"
/clone="IMAGE:8222610"
/sex="female"
/tissue_type="Cerebral cortex"
/dev_stage="8.5 months old calf"
/lab_host="E. coli DH10B T1 Phage resistant"
/clone_lib="GC_BGC-28"
/note="Organ: Cerebral cortex; Vector: pEXpress 1; Site 1: Blunt (5' end of cDNA); Site 2: NotI (3' end of cDNA)";

ORIGIN
Query Match 8.6%; Score 69; DB 10; Length 916;
Best Local Similarity 87.2%; Pred. No. 4.6e-05;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGAGGCTGTCTTACTACACCATTTTACTTCTTCTGGAATTC 685
DB 813 GCACCTGAAGAGAGAGGCTGTCTTCTTCAACACCATTTCTTCTTCTCGAGTTC 754

QY 686 ATTACTCTCTTGATAGTATGTTCTGT 711
DB 753 ATTACTCTCTTATAGATGATTTCTTT 728

RESULT 31
DV915213/c 801 bp mRNA linear EST 01-DEC-2005
LOCUS LB0287.CR_A06 GC_BGC-28 Bos taurus cDNA clone IMAGE:8222096, mRNA
DEFINITION sequence.
DV915213
VERSION DV915213.1 GI:82970965
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 801)
Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shennan, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaf, R., Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R., Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Scott, J., Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J., and Marra, M.A.
Bovine Genome Sequencing Program: Full-length cDNA Sequencing
Unpublished (2005)

TITLE
JOURNAL
COMMENT Contact: Robert Kirkpatrick
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia, Canada, V5Z 4S6

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACATTTTGTCTTTCTTCTGAATTC 685
 |||||
 DB 225 GCACCTGAAGCGAGGCTGCGCTTTTGCATCGCATTTTGTCTTTCTTCTGAGTTC 166
 |||||

QY 686 ATTACTCTCTTGTAGATTAAGTTCTGT 711
 |||||
 DB 165 ATTACTCTCTTGTAGATTAAGTTCTTT 140
 |||||

RESULT 33
 BE652295/c 543 bp mRNA linear EST 06-SEP-2000
 LOCUS UI-M-AHO-acy-e-12-0-UI.r1 NIH BMAP MCE Mus musculus cDNA clone
 DEFINITION UI-M-AHO-acy-e-12-0-UI 5', mRNA sequence.
 ACCESSION BE652295
 VERSION BE652295.1 GI:9978138
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 543)
 REFERENCE Bonaldo, M.F., Lennon, G., and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9690
 Email: mst@mail.nih.gov
 CDNA Library Preparation: M.B. Soares Lab Clone distribution:
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
 should be noted that Benco Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements The following repetitive elements were
 found in this cDNA sequence: 427-537, >(CA)nSimple_repeat
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..543
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-AHO-acy-e-12-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH BMAP MCE"
 /note="Vector: p7713D-Pac1; Site 1: Not I; Site 2: Eco RI;
 The NIH BMAP MCE library is a non-normalized library
 constructed from mouse cerebellum. The tag is a string of
 5 nucleotides present between the Not I site and the
 oligo-dT track. The library was constructed as described
 by Bonaldo, Lennon and Soares, Genome Research 6:
 791-806, 1996. Tissue provided by Ms. Annie Novakovich,
 Zivic-Miller Laboratories."

ORIGIN
 Query Match 8.6%; Score 68.4; DB 7; Length 543;
 Best Local Similarity 87.2%; Pred. No. 6e-05;
 Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACATTTTGTCTTTCTTCTGAATTC 685
 |||||
 DB 236 GCACCTGAAGCGAGGCTGCGCTTTTGCATCGCATTTTGTCTTTCTTCTGAGTTC 177
 |||||

QY 686 ATTACTCTCTTGTAGATTAAGTTCTGT 711
 |||||

DB 176 ATTACTCTCTTGTAGATTAAGTTCTTT 151
 |||||

RESULT 34
 BU743848 553 bp mRNA linear EST 21-APR-2003
 LOCUS m149d11.y1 McCarrey Eddy round spermatid Mus musculus cDNA clone
 DEFINITION IMAGE:644944.5', similar to SW:MK10_HUMAN P53779 MITOGEN-ACTIVATED
 PROTEIN KINASE 10 ; , mRNA sequence.
 ACCESSION BU743848
 VERSION BU743848.1 GI:23691967
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 553)
 REFERENCE McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
 Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,
 Ritter, E., Tsagaris, R., Ronko, I., Maguire, L., Kennedy, S.,
 Bennett, J., Waterston, R., and Wilson, R.
 NIHES Mouse
 Unpublished (2002)
 JOURNAL Contact: McCarrey/Eddy NIHES Mouse
 COMMENT NIHES Mouse
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL, contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:2093756
 Seq primer: -40RP from Gibco
 High quality sequence stop: 419.
 Location/Qualifiers
 1..553
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:644944"
 /sex="male"
 /tissue_type="round spermatids, pooled from multiple mice"
 /dev_stage="60 day"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="McCarrey Eddy round spermatid"
 /note="Organ: testis; Vector: pluescript SK+
 (Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo
 dt-primed [5'-(GA)10-ACTAGTCGAGTTTCTTTTCTT-3'] and
 directionally cloned using 5' linkers 5'-AATTCGACGAG-3'
 and 5'-CTCGGCGG-3'. Size selection of >400bp material
 gives average insert size ranging from 1-2 kb. Library was
 mass excised (from lambda-Unizap-XR) and resulting
 single-stranded phagemids were prepped and transformed
 into DH10B. Library contains 98.5% recombinants.
 References: J. Androl. 20:635-639 and Gene 25:263-269.
 Library constructed and donated by J. McCarrey, Ph.D.
 (Southwest Foundation for Biomedical Research, Dept. of
 Genetics); excision done by E.M. Eddy, Ph.D. (National
 Institutes of Health, National Institute of Environmental
 Health Sciences). Original lambda-based library is
 available through ATCC, catalog #63423."

ORIGIN
 Query Match 8.6%; Score 68.4; DB 3; Length 553;
 Best Local Similarity 87.2%; Pred. No. 6e-05;
 Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACATTTTGTCTTTCTTCTGAATTC 685
 |||||
 DB 152 GCACCTGAAGCGAGGCTGCGCTTTTGCATCGCATTTTGTCTTTCTTCTGAGTTC 93
 |||||

QY 686 ATTACTCTCTTGATAGTACTTCTGT 711
 |||||
 Db 92 ATTACCTCTTGATAGTACTTCTTT 67
 |||||

RESULT 35
 CB234404/c 763 bp mRNA linear EST 10-FEB-2003
 LOCUS AGENCOURT 11459319 NIH MGC 166 Mus musculus cDNA clone
 DEFINITION IMAGE:30247531 5', mRNA sequence.
 ACCESSION CB234404
 VERSION CB234404.1 GI:28285982
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 763)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: T. Rajendra Kumar and Martin M. Matzuk
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: NDCM06 row: f column: 20
 High quality sequence stop: 597.

FEATURES
 source
 1..763
 location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30247531"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_166"
 /note="Organ: brain; Vector: pDNR-LIB; Site 1: SfiI
 (ggccatcgcc); Site 2: SfiI (ggcgcgcgcgc);
 Non-normalized full-length enriched library 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence:
 5'-ATCTAGAGCCGACGCGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 2.05
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA) Corp."

ORIGIN
 Query Match 8.6%; Score 68.4; DB 4; Length 763;
 Best Local Similarity 87.2%; Pred. No. 6.2e-05;
 Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 626 GTCCTGAGAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGGAATTC 685
 |||||
 Db 176 GCACCTGAGAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGGAATTC 117
 |||||

QY 686 ATTACTCTCTTGATAGTACTTCTGT 711
 |||||
 Db 116 ATTACCTCTTGATAGTACTTCTTT 91
 |||||

RESULT 36
 AK042368 2343 bp mRNA linear HTC 02-SEP-2005
 LOCUS AK042368/c
 DEFINITION Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched
 library, clone:A63085G12 product:mtogen activated protein kinase

ACCESSION
 AK042368
 VERSION
 AK042368.1 GI:26335078
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL 10349636
 PUBLISHED 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL 11042159
 PUBLISHED 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Komano, H., Akiyama, J., Nishi, K., Katsunai, T., Tachiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL 11076861
 PUBLISHED 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 JOURNAL 5
 The FANTOM Consortium, the RIKEN Genome Exploration Research Group
 Phase I and II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL 6
 RIKEN Genome Exploration Research Group, Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium.
 Antisense transcription in the Mammalian Transcriptome
 Science 309, 1564-1566 (2005)
 JOURNAL 7
 The FANTOM Consortium, Riken Genome Exploration Research Group and
 Genome Science Group (Genome Network Project Core Group).
 The Transcriptional Landscape of the Mammalian Genome
 Science 309, 1559-1563 (2005)
 JOURNAL 8 (bases 1 to 2343)
 PUBLISHED 9
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirazane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komano, H., Kouda, M.,
 Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohnato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Substitution
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).


```

source
1..2729
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:9630051C24"
/db_xref="taxon:10090"
/clone="9630051C24"
/cisue_type="cerebellum"
/clone_1b="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days neonate"
1..2729
/note="Mitogen activated protein kinase 10
[MGD]MG1:1346863 [GB]NM_009158, evidence: BLASTN, 99%,
match=2139)".
putative"

misc_feature
1..2729
/note="Mitogen activated protein kinase 10
[MGD]MG1:1346863 [GB]NM_009158, evidence: BLASTN, 99%,
match=2139)".
putative"

ORIGIN
Query Match 8.6%; Score 68.4; DB 6; Length 2729;
Best Local Similarity 87.2%; Pred. No. 6,9e-05;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 626 GACCTGAAGAGAGAGGCTGTCCTTTTACTACACCATTTTGTGCTTCTTCGAAATTC 685
1774 GCACCTGAAGGAGAGGCGCTGGCTTTGACTACGCCATTTGTGCTTCTTCGATTC 1715
Db 1774 GCACCTGAAGGAGAGGCGCTGGCTTTGACTACGCCATTTGTGCTTCTTCGATTC 1715

Oy 686 ATTACTCTCTTGAGATAAGTTCTGT 711
1714 ATTACTCTCTTGAGATAAGTTCTTT 1689

RESULT 38
BF854904 561 bp mRNA linear EST 16-JAN-2001
LOCUS MRL-FN0210-301000-001-b10 FN0210 Homo sapiens CDNA, mRNA sequence.
DEFINITION BF854904
ACCESSION BF854904
VERSION BF854904.1 GI:12242648
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 561)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRkt2-MRL-FN0210-
301000-001-b10&3=2800-10-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 559.
Location/Qualifiers
1..561
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
FEATURES
source
1..561
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"

```

```

/clone.lib="FN0210"
/notes:Organ: prostate_normal, Vector: puc18, Site: 1:
SmaI, Site: 2: SmaI; A mini-library was made by cloning
products derived from ORS2ES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

```

Fletcher, C., Fujita, M., Gariboldi, M., Guertinich, S., Hill, D., Hofmann, M., Hume, D. A., Kamliya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Marzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, J., Sakamoto, N., Saeki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Borja, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S., and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
11217851

CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, O., Otsu, N., Saito, R., Suzuki, H., Yamanka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schiraldi, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chotia, C., Corbani, L. E., Cousins, S., Della, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, D., Grimmond, S., Guertinich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Borja, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayakawa, N., Hirozane-Kishikawa, T., Komori, H., Nakamura, K., Sakakume, N., Sato, K., Shiraki, T., Waki, K., Kawai, I., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, O., Birney, E. and Hayashizaki, Y.

CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420 (6915), 563-573 (2002)
12466851

CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Attalaya, R. N., Bailey, T. B., Banerji, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chin, K. P., Choudhary, V., Christofels, A., Clutterbuck, D. R., Crome, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gotohori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeno, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kimura, T., Kito, H., Kollias, G., Krishnan, S. P., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Ljun, S., McMilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morita, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakaguchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Ohtsuka, Y., Pang, K. C., Pavan, W. J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C. A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinciat, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R.,

Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegener, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamashita, H., Zdobovskiy, E., Zhu, S., Zimmer, A., Hilde, M., Bult, C., Grimmond, S. M., Teasdale, R. D., Liu, E. T., Brusic, V., Quackenbush, J., Wahlstedt, C., Matick, J. S., Hume, D. A., Kai, C., Saeki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imanura, K., Itoh, M., Kato, T., Kawai, H., Kawasawa, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Niimura, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Wataniki, A., Okamura-Ohno, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072

CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakashima, M., Nakamura, M., Nishida, H., Yap, C. C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K. C., Hallinan, J., Matick, J. S., Hume, D. A., Lipovich, L., Batalov, S., Engstrom, P. G., Mizuno, Y., Fagioni, M. A., Sandelin, A., Chalk, A. M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlstedt, C.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
16141073

CONSRTM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

8 (bases 1 to 2629)

Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Niimura, N., Nishiyori, H., Nomura, K., Ohno, M., Sakakume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wataniki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submissions

Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopaedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
Location/Qualifiers

1. 2629

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="PANTOM,DB:A730093C22"

/db_xref="taxon:10090"

/clone="A730093C22"

/tissue_type="cerebellum"

/clone_1ib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="7 days neonate"

518..1774

/note="unlabeled protein product; mitogen activated protein kinase 10 (MGD) [MG:1346863 GB|BC046625, evidence: BLAST, 99%, match=1759]

putative"

/codon_start=1

/protein_id="BAE37234.1"

/db_xref="GI:74190276"

/translation="MSLPLFLYCSFPTLDVKIAFCQCGDKVDVSSIAKHYMSKVDNQFSAVGGSTFVLKRYONLKPISGAGGICVAAADAVLDNRVAIKKSRPQNO THAKAYRELIVMKVHNKNIISLNVFTPKTLEEFDDVYVLMELPMANICOVIME LDHMRSYLVQMLCGIKHLSAGIHHDLKPSNIVVSDCTLKILDFGLARTAGTSF

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 578)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP).
Seq primer: pYX-5.
Location/Qualifiers
1. 578
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone_image="5695500"
/tissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH BMAP_EH0P"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonafio, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is CAGCCAGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemlin Chin, Ph.D., Program Coordinator."

ORIGIN
Query Match 8.2%; Score 66; DB 3; Length 578;
Best Local Similarity 87.8%; Pred. No. 0.00021;
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTTTACTACACATTTTAACTCTTCTGAAATCATTA 689
DB 335 CTGAAGAGAGAGGCTGCTTTACTACACATTTTAACTCTTCTGAAATCATTA 276
QY 690 CTTCCTTGATGATAGTTCTGT 711
DB 275 CCTCCTTGATGATAGTTCTTT 254

RESULT 43
CX221469/c 639 bp mRNA linear EST 29-DEC-2004
DEFINITION
MNS38129 Mouse Neurosphere Normalized cDNA library Mus musculus
CDNA 5', mRNA sequence.
ACCESSION
CX221469
VERSION
CX221469.1 GI:56876761
KEYWORDS
EST
SOURCE
Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
1 (bases 1 to 639)
Williams, C., Wirta, V., Lundberg, J., and Felsen, J.
TITLE
Expressed sequence tags of cDNA clones from murine neurospheres
JOURNAL
Unpublished (2005)
Contact: Williams, C.
COMMENT
Molecular Biotechnology
Institution of Biotechnology
Albano University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +4685378332.
Fax: +4685378481
Email: cecilia.williams@biotech.kth.se
Seq primer: MJ9EM.
Location/Qualifiers
1. 639
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
/tissue_type="lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"
/clone_1lb="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult Brain; Vector: pCMVSPORT6.0; A cDNA
library was constructed in pCMVSPORT6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/Resgen"

ORIGIN
Query Match 8.2%; Score 66; DB 8; Length 639;
Best Local Similarity 87.8%; Pred. No. 0.00022;
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTTTACTACACATTTTAACTCTTCTGAAATCATTA 689
DB 397 CTGAAGAGAGAGGCTGCTTTACTACACATTTTAACTCTTCTGAAATCATTA 338
QY 690 CTTCCTTGATGATAGTTCTGT 711
DB 337 CCTCCTTGATGATAGTTCTTT 316

RESULT 44
CF951683 721 bp mRNA linear EST 20-NOV-2003
DEFINITION
UI-M-HLO-cmc-a-15-0-UI_r1 NIH BMAP_HLO Mus musculus cDNA clone
IMAGE:30633902 5', mRNA sequence.
ACCESSION
CF951683
VERSION
CF951683.1 GI:38467552
KEYWORDS
EST
SOURCE
Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 721)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP).
The following repetitive elements were found in this cDNA
sequence: 409-519, >(CA)nSimple_repeat

FEATURES
Seq primer: pyx-5.
Location/Qualifiers
1. .721
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30633902"
/issue_type="Upper Head"
/dev_stage="9.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH BMAP H1.0"
/note="Organ: Head, Vector: pyx-Asc, Site 1: Ecor I, Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGACTGAAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN
Query Match 8.2%; Score 66; DB 5; Length 721;
Best Local Similarity 87.8%; Pred. No. 0.00022;
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTTACTACACCATTTTACTCTTTCTTCTGAAATCATTA 689
DB 209 CTGAAGCGGAGGCGGCGCTTTGACACGCACTTCTTCTCTTCTGAGTTCATTA 150
QY 690 CTTCCTTGTAGATAGTTCTGT 711
DB 149 CCTCCTTGTAGATAGTTCTTT 128

RESULT 45
BM943588/c 740 bp mRNA linear EST 14-MAR-2002
LOCUS UI-M-EMO-bym-m-16-0-UI.r1 NIH_BMAP_EMO Mus musculus cDNA clone
DEFINITION IMAGE:5694135 5', mRNA sequence.
ACCESSION BM943588
VERSION
KEYWORDS
SOURCE EST. BM943588.1 GI:19427173
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 740)
NIH-MGC <http://mgc.ncl.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
The following repetitive elements were found in this cDNA sequence: 498-608, >(CA)n#Simple_repeat
Seq primer: pyx-5.
Location/Qualifiers

source
1. .740
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5694135"
/issue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH BMAP EMO"
/note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCAGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match 8.2%; Score 66; DB 3; Length 740;
Best Local Similarity 87.8%; Pred. No. 0.00022;
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTTTACTACACCATTTTACTCTTTCTTCTGAAATCATTA 689
DB 298 CTGAAGCGGAGGCGGCGCTTTGACACGCACTTCTTCTCTTCTGAGTTCATTA 239
QY 690 CTTCCTTGTAGATAGTTCTGT 711
DB 238 CCTCCTTGTAGATAGTTCTTT 217

RESULT 46
CX852086 802 bp mRNA linear EST 03-AUG-2005
LOCUS JGI_CAL8222.rev NIH_XGC_tropbtrn4 Xenopus tropicalis cDNA clone
DEFINITION IMAGE:766337 3', mRNA sequence.
ACCESSION CX852086
VERSION
KEYWORDS
SOURCE EST. CX852086.2 GI:71783812
ORGANISM Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 802)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
On Feb 2, 2005 this sequence version replaced gi:56509682.
Other ESTs: JGI_CAL8222.fwd
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley)
<http://tropicalis.berkeley.edu/home>
cDNA Library Preparation: DOE Joint Genome Institute
<http://www.jgi.doe.gov>
DNA Sequencing: DOE Joint Genome Institute; <http://www.jgi.doe.gov>
Clone Distribution: I.M.A.G.E. Consortium/LLNL;

Query Match	8.0%;	Score 64;	DB 3;	Length 331;
Best Local Similarity	93.1%;	Pred. No. 0.00059;		
Matches 67;	Conservative 5;	Mismatches 0;	Gaps 0;	

QY 630 CTGAGAGAGAGGCTGCTTTTACTACACATTTCCTTTCTTCTGATCTTA 689
 DB 72 CTGAGAGAGATGGCTGCTTTTACTACACATTTCCTTTCTTCTGATCTTA 13
 QY 690 CTTCCTGTAGA 701
 DB 12 CTTCCTGTAGA 1

RESULT 49
 BU725204 778 bp mRNA linear EST 09-MAR-2004
 LOCUS BU725204 MF01FFA cDNA Oryzias latipes cDNA clone MF01FFA035b01 3',
 DEFINITION mRNA sequence.
 ACCESSION BU725204 GI:45266296
 VERSION BU725204.1 GI:45266296
 KEYWORDS EST.
 SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Oryzias latipes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Perciforma; Atherinomorpha;
 Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
 1 (bases 1 to 778)
 Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
 Medaka EST Project in Takeda's lab
 Unpublished (2001)
 Contact: Tadasi Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source location/Qualifiers
 1..778
 /organism="Oryzias latipes"
 /mol_type="mRNA"
 /strain="Md-RR"
 /db_xref="taxon:8090"
 /clone="MF01FFA035b01"
 /sex="mixture of female and male"
 /tissue_type="whole embryo"
 /dev_stage="fry stage 40"
 /clone_id="MF01FFA cDNA"

ORIGIN
 Query Match 7.4%; Score 59; DB 2; Length 778;
 Best Local Similarity 74.7%; Pred. No. 0.0089;
 Matches 74; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 613 TCACGAGAGTGAAGTCTGAGAGAGAGGCTGCTTTTACTACACATTTCCTT 672
 DB 183 TTATGACACTGAGAGTGAAGTGAAGGCTGCTTCCTTCAACAAGCATTTCGTTCT 242
 QY 673 TTCTTCTGAATTCATTCTCTCTGTAGATTAAGTTCTGT 711
 DB 243 CTCCTCAAGTCAATGACCTCTTTGTAGATTAGTTCTTT 281

RESULT 50
 CX143962 645 bp mRNA linear EST 03-JAN-2005
 LOCUS CX143962 NCCGWA 03RT Oncorhynchus mykiss cDNA 3', mRNA sequence.
 DEFINITION 1283656 NCCGWA 03RT Oncorhynchus mykiss cDNA 3', mRNA sequence.
 ACCESSION CX143962
 VERSION CX143962.1 GI:57000617
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 645)

AUTHORS Rexroad, C.E., Rise, M., Koop, B., von Schalburg, K. and Yao, J.
 TITLE 03RT rdb, NCCGWA/WVU EST Project, Phase II, in collaboration with GRASP
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccgwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Place: 116 row: J column: 6
 Seq primer: GTATATGACCTCACTATGAGG.
 Location/Qualifiers
 1..645
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_id="NCCGWA 03RT"
 /note="Vector: pBluescript SK+; This is a normalized (Coc = 5) O. mykiss whole juvenile library created by Matthew L. Rise from approximately 4 month old O. mykiss (Tzenzai-cut Lake strain) obtained from Vancouver Island Trout Hatchery (Duncan, B.C.)."

ORIGIN
 Query Match 7.0%; Score 55.8; DB 8; Length 645;
 Best Local Similarity 72.7%; Pred. No. 0.048;
 Matches 72; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 613 TCACGAGAGTGAAGTCTGAGAGAGAGGCTGCTTTTACTACACATTTCCTT 672
 DB 201 TTATGACACTGAGAGTGAAGTGAAGGCTGCTTCCTTCAACAAGCATTTCGTTCT 142
 QY 673 TTCTTCTGAATTCATTCTCTCTGTAGATTAAGTTCTGT 711
 DB 141 CTCCTCAAGTCAATGACCTCTTTGTAGATTAGTTCTTT 103

Search completed: July 19, 2006, 20:15:06
 Job time : 4924 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 18:46:15 ; Search time 204 Seconds
(without alignments)
7337.682 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 1 acattcttaaacctctta.....caataactgcttgatg 800

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/ina/1.COMB.seq:*
- 2: /EMC_Celerra_SIDS3/prodata/2/ina/5.COMB.seq:*
- 3: /EMC_Celerra_SIDS3/prodata/2/ina/6.COMB.seq:*
- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6.COMB.seq:*
- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7.COMB.seq:*
- 6: /EMC_Celerra_SIDS3/prodata/2/ina/H.COMB.seq:*
- 7: /EMC_Celerra_SIDS3/prodata/2/ina/PCBUS.COMB.seq:*
- 8: /EMC_Celerra_SIDS3/prodata/2/ina/RE.COMB.seq:*
- 9: /EMC_Celerra_SIDS3/prodata/2/ina/Backfile1.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	82.8	10.3	1422	3	US-09-909-650B-24
2	82.8	10.3	1505	3	US-09-130-616-178
3	82.8	10.3	1505	3	US-09-023-655-952
4	82.8	10.3	1505	3	US-09-165-522-1
5	82.8	10.3	2367	3	US-09-165-522-3
6	82.8	10.3	2677	3	US-09-566-921-14
7	80.4	10.1	1306	3	US-09-909-650B-22
8	80.4	10.1	1773	3	US-09-130-616-177
9	80.4	10.1	1773	3	US-09-165-522-4
10	80.4	10.1	2131	3	US-09-771-161A-87
11	80.4	10.1	2372	3	US-09-130-616-174
12	80.4	10.1	2372	3	US-09-016-434-1389
13	80.4	10.1	2372	3	US-09-165-522-6
14	80.4	10.1	2372	3	US-09-165-522-7
15	80.4	10.1	2982	3	US-09-566-921-133
16	66.8	8.3	1975	3	US-09-130-616-175
17	66.8	8.3	1975	3	US-09-165-522-9
18	64.4	8.1	2522	3	US-09-130-616-176
19	64.4	8.1	2522	3	US-09-165-522-11
20	55.8	7.0	48313	3	US-09-949-016-17088
21	48.8	6.1	2372	3	US-09-130-616-165
22	48.8	6.0	1619	3	US-10-104-047-1930
23	48.4	6.0	1619	3	US-09-130-616-173

24	48.4	6.0	1780	3	US-08-230-602B-17	Sequence 17, Appl
25	48.4	6.0	1780	3	US-09-861-012A-17	Sequence 17, Appl
26	48.4	6.0	1780	3	US-09-861-098A-17	Sequence 17, Appl
27	48.4	6.0	1780	3	US-09-861-097-17	Sequence 17, Appl
28	48.4	6.0	1780	7	PCT-US94-12913A-17	Sequence 17, Appl
29	48.4	6.0	1782	3	US-09-209-668-16	Sequence 16, Appl
30	48.4	6.0	1782	3	US-09-130-616-169	Sequence 169, Appl
31	48.4	6.0	132456	3	US-09-949-016-13750	Sequence 13750, A
32	46.8	5.8	1352	3	US-09-130-616-171	Sequence 171, Appl
33	46.8	5.8	1352	3	US-09-023-655-953	Sequence 953, Appl
34	46.8	5.8	1392	3	US-09-949-016-5346	Sequence 5346, Appl
35	46.8	5.8	1523	3	US-09-130-616-172	Sequence 172, Appl
36	46.8	5.8	1769	2	US-08-253-155A-19	Sequence 19, Appl
37	46.8	5.8	1873	3	US-09-016-434-1437	Sequence 1437, Appl
38	46	5.8	601	3	US-09-949-016-53117	Sequence 53117, A
39	46	5.8	1141	3	US-09-806-708B-22	Sequence 22, Appl
40	46	5.8	100877	3	US-09-949-016-13276	Sequence 13276, A
41	45.6	5.7	601	3	US-09-949-016-53116	Sequence 53116, A
42	44.6	5.6	832	3	US-09-621-976-2813	Sequence 2813, Appl
43	44.4	5.5	1349	3	US-09-130-616-168	Sequence 168, Appl
44	44.4	5.5	1365	3	US-09-130-616-166	Sequence 166, Appl
45	44.4	5.5	1365	3	US-09-016-434-1139	Sequence 1139, Appl
46	42.4	5.3	832	3	US-09-621-976-2813	Sequence 2813, Appl
47	42.4	5.3	1311	3	US-09-130-616-167	Sequence 167, Appl
48	42	5.2	1418	3	US-09-209-668-14	Sequence 14, Appl
49	42	5.2	1418	3	US-09-130-616-164	Sequence 164, Appl
50	42	5.2	1418	3	US-08-220-602B-11	Sequence 11, Appl
51	42	5.2	1418	3	US-09-861-012A-11	Sequence 11, Appl
52	42	5.2	1418	3	US-09-861-098A-11	Sequence 11, Appl
53	42	5.2	1418	3	US-09-861-097-11	Sequence 11, Appl
54	42	5.2	1418	7	PCT-US94-08119-11	Sequence 11, Appl
55	42	5.2	1418	7	PCT-US94-12913A-11	Sequence 11, Appl
56	42	5.2	1514	3	US-09-949-016-2008	Sequence 2008, Appl
57	42	5.2	1893	3	US-09-417-197-62	Sequence 44, Appl
58	42	5.2	1902	3	US-09-417-197-44	Sequence 1, Appl
59	42	5.1	640681	3	US-08-790-988-1	Sequence 50, Appl
60	41	5.1	1908	3	US-08-845-558-50	Sequence 50, Appl
61	40.8	5.1	1908	3	US-08-845-558-50	Sequence 50, Appl
62	40.8	5.1	1908	3	US-09-228-784A-50	Sequence 50, Appl
63	40.8	5.1	1908	3	US-09-569-098A-4	Sequence 4, Appl
64	40.8	5.1	1908	3	US-09-569-098A-50	Sequence 50, Appl
65	40.8	5.1	1908	3	US-08-845-558-4	Sequence 4, Appl
66	40.8	5.1	1991	3	US-08-990-571-4	Sequence 4, Appl
67	40.8	5.1	1991	3	US-08-723-142A-4	Sequence 4, Appl
68	40.8	5.1	1991	3	US-09-528-784A-4	Sequence 4, Appl
69	40.8	5.1	1991	3	US-09-569-098A-4	Sequence 4, Appl
70	40.8	5.1	50000	3	US-09-662-254B-26	Sequence 26, Appl
71	40.8	5.1	134987	3	US-09-949-016-15348	Sequence 15348, A
72	40.8	5.1	134987	3	US-09-949-016-15349	Sequence 15349, A
73	40.8	5.1	134987	3	US-09-949-016-15350	Sequence 15350, A
74	40.8	5.1	134987	3	US-09-949-016-15357	Sequence 15357, A
75	40.8	5.1	134987	3	US-09-949-016-15508	Sequence 15508, A
76	40.8	5.1	134987	3	US-09-949-016-15509	Sequence 15509, A
77	40.6	5.1	105679	3	US-09-949-016-12360	Sequence 12360, A
78	40.4	5.0	1582	3	US-08-545-196B-10	Sequence 10, Appl
79	40.4	5.0	1582	3	US-08-545-196B-12	Sequence 12, Appl
80	40.4	5.0	1582	5	US-09-109-082A-10	Sequence 10, Appl
81	40.4	5.0	1582	5	US-09-109-082A-12	Sequence 12, Appl
82	40.4	5.0	238815	3	US-09-949-016-14574	Sequence 16274, A
83	40	5.0	260266	3	US-09-949-016-17037	Sequence 17037, A
84	40	5.0	260266	3	US-09-949-016-12106	Sequence 12106, A
85	40	5.0	786431	3	US-09-751-389-3	Sequence 3, Appl
86	39.6	5.0	3355	3	US-09-774-528-5	Sequence 5, Appl
87	39.6	5.0	3355	3	US-10-120-988-5	Sequence 5, Appl
88	39.4	4.9	540	3	US-09-662-254B-62	Sequence 62, Appl
89	39.4	4.9	1452	3	US-09-248-796A-3739	Sequence 3739, Appl
90	39.2	4.9	601	3	US-09-949-016-14584	Sequence 14584, A
91	39.2	4.9	175265	3	US-09-949-016-15830	Sequence 15830, A
92	39.2	4.9	192506	3	US-09-328-352-2679	Sequence 2679, Appl
93	38.8	4.8	991	3	US-09-790-988-1	Sequence 1, Appl
94	38.8	4.8	640681	3	US-09-949-016-68185	Sequence 68185, A
95	38.4	4.8	601	3	US-09-949-016-68185	Sequence 68185, A
96	38.4	4.8	1755	3	US-09-248-796A-3448	Sequence 3448, Appl

C 97 38.4 4.8 32392 3 US-09-662-254B-27 Sequence 27, Appl
C 98 38.4 4.8 156324 3 US-09-949-016-13749 Sequence 13749, A
C 99 38 4.8 601 3 US-09-949-016-68481 Sequence 68481, A
C 100 38 4.8 130724 3 US-09-949-016-13753 Sequence 13753, A

ALIGNMENTS

RESULT 1

US-09-909-650B-24/c
Sequence 24, Application US/09090650B
Patent No. 6649388
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Inc.
APPLICANT: Fournier, Alain
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
APPLICANT: Desautels-Cremond, Francine
TITLE OF INVENTION: Polypeptides Derived From JNK3
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650B
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 1422
TYPE: DNA
ORGANISM: homo sapiens
US-09-909-650B-24

Query Match 10.3%; Score 82.8; DB 3; Length 1422;
Best Local Similarity 97.7%; Pred. No. 4e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGAAATTC 685
DB 1283 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGAAATTC 1224
QY 686 ATTACTCTCTGTAGATTAAGTTCTGT 711
DB 1223 ATTACTCTCTGTAGATTAAGTTCTTT 1198

RESULT 2

US-09-130-616-178/c
Sequence 178, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monla, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 178
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapien
US-09-130-616-178

Query Match 10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 4.1e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGAAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGAAATTC 1264
QY 686 ATTACTCTCTGTAGATTAAGTTCTGT 711
DB 1263 ATTACTCTCTGTAGATTAAGTTCTTT 1238

RESULT 3

US-09-023-655-952/c
Sequence 952, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 952:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G1463124
US-09-023-655-952

Query Match 10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 4.1e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGAAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTACTCTTCTGAAATTC 1264
QY 686 ATTACTCTCTGTAGATTAAGTTCTGT 711

```

Db      1263 ATTACTTCCTGTGATAGTAAGTTCTTT 1238

RESULT 4
US-09-165-522-1/c
; Sequence 1, Application US/09165522
; Patent No. 6943000
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
            Flavel, Richard A.
            Rakic, Paeko
            Whitmarsh, Alan
            Kuan, Chia-yi
            Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 68...1459
US-09-165-522-1
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
Query Match      10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 4,1e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626 GTACCTGAAGGAGGAGCGTCGTCCTTTTACTACACCATTTTGTCTTTCTTCGGAATTC 685
      |||
Db      1323 GCACCTGAAGGAGGAGGCGTCGTCCTTTTACTACACCATTTTGTCTTTCTTCGGAATTC 1266
      |||
QY      686 ATTACTTCCTGTGATAGTAAGTTCTTT 711
      |||
Db      1263 ATTACTTCCTGTGATAGTAAGTTCTTT 1238
      |||

RESULT 5
US-09-165-522-3/c
; Sequence 3, Application US/09165522
; Patent No. 6943000
GENERAL INFORMATION:

```

```

1  APPLICANT: Davis, Roger J.
2  Flavel, Richard A.
3  Rakic, Pasko
4  Whitmarsh, Alan
5  Kuan, Chia-Yi
6  Yang, Di
7  TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
8  NUMBER OF SEQUENCES: 24
9  CORRESPONDENCE ADDRESS:
10 ADDRESSSEE: Fish & Richardson P. C.
11 STREET: 225 Franklin Street
12 CITY: Boston
13 STATE: MA
14 COUNTRY: USA
15 ZIP: 02110-2804
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette
18 COMPUTER: IBM Compatible
19 OPERATING SYSTEM: Windows 95
20 SOFTWARE: PASCSEQ for Windows Version 2.0b
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/165,522
23 FILING DATE: 02-Oct-1998
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 60/060,995
26 FILING DATE: 03-Oct-1997
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Fasse, J. Peter
29 REGISTRATION NUMBER: 32,983
30 REFERENCE/DOCKET NUMBER: 10363/005001
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 617/542-5070
33 TELEFAX: 617/542-8906
34 TELEX: 200154
35 INFORMATION FOR SEQ ID NO: 3:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 2367 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: double
40 TOPOLOGY: linear
41 MOLECULE TYPE: DNA
42 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
43 US-09-165-522-3
44
45 Query Match 10.3%; Score 82.8; DB 3; Length 2367;
46 Best Local Similarity 97.7%; Pred. No. 4.6e-11;
47 Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
48
49 QY 626 GTACCTTAAGAGAGAGGCTGTCTTTACTTACACACATTTTAAAGCTTTCTTCGAAATTC 685
50 DB 1479 GCACCTTAAGAGAGAGGCTGTCTTTACTTACACACATTTTAAAGCTTTCTTCGAAATTC 1420
51 QY 686 ATTACTTCCTGTGATGATGTTCTGT 711
52 DB 1419 ATTACTTCCTGTGATGATGTTCTTT 1394
53
54 RESULT 6
55 US-09-566-921-34/C
56 Sequence 34, Application US/09566921
57 Patent No. 6682888
58 GENERAL INFORMATION:
59 APPLICANT: Loring, Jeanne F.
60 APPLICANT: Tinsley, Debora W.
61 APPLICANT: Edwards, Carla M.
62 TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
63 FILE REFERENCE: PA-0024 US
64 CURRENT APPLICATION NUMBER: US/09/566,921
65 CURRENT FILING DATE: 2000-05-05
66 NUMBER OF SEQ ID NOS: 138
67 SOFTWARE: PERL Program
68 SEQ ID NO 34
69 LENGTH: 2677

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyle ID No. 6682888 413797.5
; NAME/KEY: unsure
; LOCATION: 2024
; OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-34

Query Match
Best Local Similarity 97.7%; Pred. No. 4.8e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAGAGAGAGGCTGTCTTACTACACCATTTTACTCTTCTTCTGAAATTC 685
DB 1795 GCACCTGAGAGAGAGGCTGTCTTACTACACCATTTTACTCTTCTTCTGAAATTC 1736
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 1735 ATTACTCTCTGTAGATAGTTCTTT 1710

RESULT 7
US-09-909-650B-22/c
; Sequence 22, Application US/09909650B
; Patent No. 6649388
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Fournier, Alain
; APPLICANT: Maury, Isabelle
; APPLICANT: Zhou-Liu, Qing
; APPLICANT: Desautels-Cremont, Francine
; TITLE OF INVENTION: Polypeptides Derived From JNK3
; FILE REFERENCE: ST99003-US-CNT-1
; CURRENT APPLICATION NUMBER: US/09/909,650B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/FR00/00104
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/122,175
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 99/00586
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
; LENGTH: 1306
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-909-650B-22

Query Match
Best Local Similarity 98.8%; Pred. No. 1.6e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTCTTCTTCTGAAATTA 689
DB 1279 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTCTTCTTCTGAAATTA 1220
QY 690 CTTCCTGTAGATAGTTCTGT 711
DB 1219 CTTCCTGTAGATAGTTCTTT 1198

RESULT 8
US-09-130-616-177/c
; Sequence 177, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
```

```

; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 177
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-130-616-177

Query Match
Best Local Similarity 98.8%; Pred. No. 1.7e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTCTTCTTCTGAAATTA 689
DB 1343 CTGAGAGAGAGGCTGTCTTACTACACCATTTTACTCTTCTTCTGAAATTA 1284
QY 690 CTTCCTGTAGATAGTTCTGT 711
DB 1283 CTTCCTGTAGATAGTTCTTT 1262

RESULT 9
US-09-165-522-4/c
; Sequence 4, Application US/09165522
; Patent No. 6943000
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Flavell, Richard A.
; APPLICANT: Rakic, Pasko
; APPLICANT: Wilmarsch, Alan
; APPLICANT: Kuan, Chia-Yi
; APPLICANT: Yang, Di
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,522
; FILING DATE: 02-Oct-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,995
; FILING DATE: 03-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 10363/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1773-base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```


MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 92...1357
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-165-522-4

Query Match 10.1%; Score 80.4; DB 3; Length 1773;
Best Local Similarity 98.8%; Pred. No. 1.7e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTCTTCTTCTTGAATTCATTA 689
DB 1343 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTCTTCTTCTTGAATTCATTA 1284
QY 690 CTTCCTTTGATAGATAGTTCTGT 711
DB 1283 CTTCCTTTGATAGATAGTTCTTT 1262

RESULT 10
US-09-771-161A-87/c
Sequence 87, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 115619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 87
LENGTH: 2131
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: -
LOCATION: (1)..(2131)
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-87

Query Match 10.1%; Score 80.4; DB 3; Length 2131;
Best Local Similarity 98.8%; Pred. No. 1.8e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTCTTCTTCTTGAATTCATTA 689
DB 1225 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTCTTCTTCTTGAATTCATTA 1166
QY 690 CTTCCTTTGATAGATAGTTCTGT 711
DB 1165 CTTCCTTTGATAGATAGTTCTTT 1144

RESULT 11
US-09-130-616-174/c
Sequence 174, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Netro, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 174
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
US-09-130-616-174

Query Match 10.1%; Score 80.4; DB 3; Length 2372;
Best Local Similarity 98.8%; Pred. No. 1.8e-10;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTCTTCTTCTTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGCGTCTCTTCTTACTACACCATTTTCTTCTTCTTGAATTCATTA 1416
QY 690 CTTCCTTTGATAGATAGTTCTGT 711
DB 1415 CTTCCTTTGATAGATAGTTCTTT 1394

RESULT 12
US-09-016-434-1389/c
Sequence 1389, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1389:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9468150
US-09-016-434-1389


```

; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 165
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-130-616-165

Query Match
Best Local Similarity 74.4%; Score 50.8; DB 3; Length 1408;
Matches 64; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1317 GCACCTAAAGAGAGCGCTGCCCTTATGACGCCATTCTTAGTTCGCTCCCAATTC 1258
QY 686 ATTACTTCTTGTAGATAAGTTCTGT 711
DB 1257 ATGACCTCTTGTATATCAGTTCTTT 1232

RESULT 22
US-10-104-047-1930/C
; Sequence 1930, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1930

Query Match
Best Local Similarity 70.7%; Score 48.8; DB 3; Length 2372;
Matches 65; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1382 GCACCTAAAGAGAGGCTGCCCTTATATCATTCTTGTCTCTCCCAAGTTC 1323
QY 686 ATTACTTCTTGTAGATAAGTTCTGAAGAA 717
DB 1322 ATACTTCTTATATATCATTTCTGAAGAA 1291

RESULT 23
US-09-130-616-173/C
; Sequence 173, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER APPLICATION NUMBER: 08/910,629
```

```

; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 173
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-173

Query Match
Best Local Similarity 74.4%; Score 48.4; DB 3; Length 1619;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTCATTA 689
DB 1172 CTGACTGAAGGCTGATCTTTTACACACCATTTGCTTCTTCCCAATTCATGA 1113
QY 690 CTTCCTTGTAGATAAGTTCTGT 711
DB 1112 CTTCCTTGTAAATTAAGTCTTT 1091

RESULT 24
US-08-220-602B-17/C
; Sequence 17, Application US/08220602B
; Patent No. 6514745
; GENERAL INFORMATION:
; APPLICANT: KARIN, MICHAEL
; APPLICANT: DAVIS, ROGER
; APPLICANT: MASAHIKO, HIBI
; APPLICANT: ANNING, LIN
; APPLICANT: DERJARD, BENOIT
; TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,602B
; FILING DATE: 25-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.,
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/015001 (PD3205)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: JNK2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59..1330
US-08-220-602B-17

Query Match
Best Local Similarity 74.4%; Score 48.4; DB 3; Length 1780;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```

QY	Db	QY	Db
630	CTGAAGGAAGAGCGCTGCTCTTTTACCAACCCATTTTGTCTTTCTCTGAATCATTA	689	
1196	CTGCATCGAAGGCTGATCTTTTACAACACCCATTTCTGTTCTTTCTTCCCAATCACA	1133	
690	CTTCCTGTAGATAGTCTGCT	711	
1136	CTTCCTTGTAAATTAGCTCTTT	1115	

RESULT 25
US-09-861-012A-17/c

```

? Sequence 17 Application US/09861012A
? Patent No. 6706509
? GENERAL INFORMATION:
? APPLICANT: KARIN, Michael
? APPLICANT: DAVIS, Roger
? APPLICANT: HIBI, Masahiko
? APPLICANT: LIN, Aning
? APPLICANT: DERIJARD, Benoit
? TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
? FILE REFERENCE: REGEN1120-12
? CURRENT APPLICATION NUMBER: US/09/861,012A
? CURRENT FILING DATE: 2001-05-18
? PRIOR APPLICATION NUMBER: US 08/220,602
? PRIOR FILING DATE: 1994-03-25
? PRIOR APPLICATION NUMBER: US 08/094,533
? PRIOR FILING DATE: 1993-07-19
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 17
? LENGTH: 1780
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (59)..(1330)
? OTHER INFORMATION:
? US-09-861-012A-17

```

Query Match	6.0%	Score 48.4;	DB 3;	Length 1780;
Best Local Similarity	74.4%;	Pred. No. 0.017;		
Matches	61;	Conservative	0;	Mismatches 21;
				Indels 0

QY	Db
630	CTGAGAGAGAAGCGCTGCTCCCTTTTACTACACCATTTTGTCTTTCTCTGAATTCATTA 689
1196	CTGATCTGGAAGCTGATCTTTTACAACACATCTTGCTCTTTCTTCCCAATCCACAGA 1137
690	CTTCTCTGTAGATTAAGTTCTGT 711
1136	CTTCTTTGTAAATTAGCTTTT 1115

RESULT 26
US-09-861-098A-17/c

Sequence 17, Application US/09861098A
Patent No. 6846644
GENERAL INFORMATION:
APPLICANT: KARIN, Michael
APPLICANT: DAVIS, Roger
APPLICANT: HIBI, Masahiko
APPLICANT: LIN, Aiming
APPLICANT: DERJUHAD, Benoit
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
FILE REFERENCE: REGEN1120-10
CURRENT APPLICATION NUMBER: US/09/861,098A
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 08/220,602
PRIOR FILING DATE: 1994-03-25
PRIOR APPLICATION NUMBER: US 08/094,533
PRIOR FILING DATE: 1993-07-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1

```

; SEQ ID NO 17
; LENGTH: 1780
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(1330)
; OTHER INFORMATION:
US-09-861-098A-17 .

```

Query Match	6.0%;	Score 48.4;	DB 3;	Length 1780;
Best Local Similarity	74.4%;	Pred. No. 0.017;		

Oy	630	CTGAAGGAGAAGCGTGTCCCTTTACTACACCAATTTTAGCTTTTTCTTGAAATTACA	689
Dd	1196	CTGCATCTGAAGCGTGATCTTTTACAACACCAATCTTGCTTTCTTCCCACATCARGA	1137
Oy	690	CTTCCTTGTAGATAGTTCTGT	711
Dd	1136	CTTCTTTGTAAATTAAGCTCTTT	1115

RESULT 27

US-09-861-097-111C
Sequence 17, Application US/09861097
Patent No. 686388
GENERAL INFORMATION:
APPLICANT: KARIN, MICHAEL
DAVIS, ROGER
MASAHITO, HIRI
ANNING, LIN
DERJARD, BENOIT
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,097
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,602
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.,
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/015001(PD3205)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1780 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: JNK2
FEATURE:
NAME/KEY: CDS
LOCATION: 59..1330

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-861-097-17

Query Match 6.0%; Score 48.4; DB 3; Length 1780;
Best Local Similarity 74.4%; Pred. No. 0.017;

Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGATTCATTA 689
DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTTCTTCCATTCATGA 1137

OY 690 CTTCCTTGATGATTAAGTCTGT 711
DB 1136 CTTCCTTGATTAATTAAGCTCTT 1115

RESULT 28

PCT-US94-12913A-17/c

Sequence 17, Application PC/RUS9412913A

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: KARIN, MICHAEL

APPLICANT: DAVIS, ROGER

APPLICANT: HIBI, MASAHIKO

APPLICANT: LIN, ANNING

TITLE OF INVENTION: ONCOROTHEIN PROTEIN KINASE

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, SUITE 500
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/12913A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/08119

FILING DATE: 18-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: LISA A. HAILE, PH.D.

REGISTRATION NUMBER: P-38,347

REFERENCE/DOCKET NUMBER: FD-3205

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 1780 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: JNK2

FEATURE:

NAME/KEY: CDS

LOCATION: 59..1330

PCT-US94-12913A-17

Query Match

Best Local Similarity 74.4%;

Matches 61; Conservative 0;

Mismatches 21; Indels 0;

Gaps 0;

Score 48.4; DB 3; Length 1780;

QY 630 CTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGATTCATTA 689

DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTTCTTCCATTCATGA 1137

OY 690 CTTCCTTGATGATTAAGTCTGT 711
DB 1136 CTTCCTTGATTAATTAAGCTCTT 1115

RESULT 29

US-09-209-668-16/c

Sequence 16, Application US/09209668A

Patent No. 6114517

GENERAL INFORMATION:

APPLICANT: MONIA, BRETT P.

APPLICANT: XU, XIAOXING S.

TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR

FILE REFERENCE: ISPH-0336

CURRENT APPLICATION NUMBER: US/09/209,668A

CURRENT FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 16

LENGTH: 1782

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (59)..(1333)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: U13951/Genbank

DATABASE ENTRY DATE: 1994-12-06

US-09-209-668-16

Query Match

Best Local Similarity 74.4%;

Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Score 48.4; DB 3; Length 1782;

QY 630 CTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTGTCTTTCTTCTGATTCATTA 689

DB 1196 CTGCATCTGAAGGCTGATCTTTTACACACCATTTCTTCTTCCATTCATGA 1137

OY 690 CTTCCTTGATGATTAAGTCTGT 711

DB 1136 CTTCCTTGATTAATTAAGCTCTT 1115

RESULT 30

US-09-130-616-169/c

Sequence 169, Application US/09130616C

Patent No. 6221850

GENERAL INFORMATION:

APPLICANT: MCKAY, ROBERT A.

APPLICANT: DEAN, NICHOLAS M.

APPLICANT: MONIA, BRETT

APPLICANT: NERO, PAM

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS

FILE REFERENCE: ISPH-0318

CURRENT APPLICATION NUMBER: US/09/130,616C

CURRENT FILING DATE: 1998-08-07

EARLIER APPLICATION NUMBER: 08/910,629

NUMBER OF SEQ ID NOS: 178

SEQ ID NO 169

LENGTH: 1782

TYPE: DNA

ORGANISM: Homo sapiens

US-09-130-616-169

Query Match

Best Local Similarity 74.4%;

Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Score 48.4; DB 3; Length 1782;

Best Local Similarity 74.4%; Pred. No. 0.017;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 630 CTGAGAGAGAGAGGCTGCTCTTTACTACACCAATTTTAGCTTTCTTCTGAAATTCATTA 689
1196 CTCATCTCTGAAGGCTGATCTTTTACACACATCTTCTGCTTTCTTCCCAATCCATGA 1137
QY 690 CTTCCTGTAGATTAAGTCTTGT 711
1136 CTCTTGTGTAAATTAAGCTCTTT 1115
Db
RESULT 31
US-09-949-016-13750/C
Sequence 13750, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13750
LENGTH: 132456
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(132456)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13750
Query Match
Best Local Similarity 71.1%; Pred. No. 0.055;
Matches 64; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 628 ACCTGAGAGAGAGGCTGCTCTTTACTACACCAATTTTAGCTTTCTTCTGAAATTCAT 687
126588 ACCTAAGAGAGAGGCTGCGCCCGCTATTACTCATCTTGTCTCTCCCAAGTCAT 126529
Db
QY 688 TACTTCTGTAGATTAAGTCTTCTTCTGAGAA 717
126528 AACTTCTTATATATCAATCTTGTAAAGA 126499
Db
RESULT 32
US-09-130-616-171/C
Sequence 171, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Garde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 171

LENGTH: 1392
TYPE: DNA
ORGANISM: Homo sapiens
US-09-130-616-171
Query Match
Best Local Similarity 5.8%; Score 46.8; DB 3; Length 1392;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 638 GAAGGCTGCTTTACTACACCAATTTTAGCTTTCTTCTGAAATTCATTAAGTCTTGT 697
1174 GAAGGCTGATCTTTTACACACATCTTGTCTTCTTCCCAATCCATTAAGTCTTGT 1115
Db
QY 698 TAGATTAAGTCTTGT 711
1114 TAAATTAAGCTCTTT 1101
Db
RESULT 33
US-09-023-655-953/C
Sequence 953, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 953:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: 91463128
US-09-023-655-953
Query Match
Best Local Similarity 5.8%; Score 46.8; DB 3; Length 1392;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 638 GAAGGCTGCTTTACTACACCAATTTTAGCTTTCTTCTGAAATTCATTAAGTCTTGT 697
1114 TAAATTAAGCTCTTT 1101
Db

NUMBER OF SEQUENCES: 1490

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1437:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9607785
US-09-016-434-1437

Query Match
Best Local Similarity 73.2%; Score 46.8; DB 3; Length 1873;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 630 CTGAGAGAGAGGCTCTCTTCTTACTACACCATTTTCTTCTTCTGCAATTATTA 689
DB 1289 CTGCATCTGAGAGGCTGATCTTTTACACACCATTTCTTCTTCTTCCATTCATGA 1230
QY 690 CTTCTCTGTAGATAGTCTGT 711
DB 1229 CTTCTTGTAAATTAAGCTCTTT 1208

RESULT 38
US-09-949-016-53117/c
Sequence 53117, Application US/09949016
Patent No. 6812338
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949, 016
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53117
LENGTH: 601
TYPE: DNA
```

```

ORGANISM: Human
US-09-949-016-53117

Query Match
Best Local Similarity 54.0%; Score 46; DB 3; Length 601;
Matches 94; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 389 ATTACTATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 448
DB 519 AATACCTTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 460
QY 449 CAGAAATGATGCCACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
DB 459 TTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400
QY 509 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562
DB 399 AATATGACTTATTATTCTTCACTGCGCTAATCTTAAGTCAATGCAATTAATCTTGA 346

RESULT 39
US-09-806-708B-22
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
PRIORITY FILING DATE: 2001-04-03
PRIORITY APPLICATION NUMBER: US 60/147,133
PRIORITY FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent In version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. FAEI promoters
US-09-806-708B-22

Query Match
Best Local Similarity 11.0%; Score 46; DB 3; Length 1141;
Matches 85; Conservative 284; Mismatches 400; Indels 2; Gaps 2;

QY 18 TTATAGTGAAGACATAGCTCTTGAAGAAAAATATATAGCATTAATTAATTAATGTCTC 77
DB 115 TTKMGKTGMRHRHWRWRAMBDDVDDHVVYTAANNATVTCMDKDKRTRMWKKNNATG 174
QY 78 AAGTATGTAAGACATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
DB 175 WDDTGTTHMNNNGBYITWVRYKTDMSBKNNYGMWKKNNYDVTYVWVWDDMC 234
QY 137 TAGATCTGTGCTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 196
DB 235 KRYVRWRTGTRGMRNVVAVMBTAHRRRYNNGWBTAMVYRVTWNNNNNNNANAMCRAY 294
QY 197 GGTATATGTTCAATATATGTCACATCAACCTTGAAGAGAGTCAACCACTAAGATGAA 256
DB 295 WGMNBAVNSTCTTWKSKTKVRISCMANNCBAGDANKDKWKKSAAMGVWNNNNNNN 354
QY 257 TGAGGAGAGAGTACCGCTGAAGAGATTAAGATGATGATGATGATGATGATGATGATGATGAT 316
DB 355 WTKKABHBAHMDVWWSAMKKHANAHSKKTBYKRTKTVNNNNNGTTWKKWMAWY 414
QY 317 GGGCATTAATGCTGAAATTTTGAATGAGGACATTAACCTTGAAGCAATGTAACATT 376
DB 415 WMDMDWEGTVNNNNNGRTYVGTWKNKMMTYVYKNNKNNCRAMDKTKTHNNNTWKK 474
QY 377 TCTCAGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 436
```

```

Db      475 MKTYMNNCYMWSMTNGKSHREBAALVVTWYMMWRVYAHANNNNNDYWMKQCTHYKYBVS 534
      437 CATCAGAATATATCGAATGTAATGCCACATGAAATATCAAAAGAAATATAAATCAAT 496
      535 KMMNNYAAWYTKSSWNTSRYYRWKTNWSWERSDTSMGRLANNYAABHGYKMTNRMW 594
      497 TATAAGACACAACCATGTGATATTGTCATCGCTGCTTTAAGCAATGTATGTATT 556
      595 BMSHTHBHBAAGAAHYMBMBYBAKCMKAMYAKKYAAGAGSNNNNNNNNNNNNNNNN 654
      557 CTTCGACCCCTACACAAAGGCCAAGAAATTAACAAGTACTAGTTATGTTATTCAC 616
      655 ATCABDDYAAASRYAAANAAMKMYYYKBAANNAAYTHANNWGCNNNAATDRRTWKNNN 714
      617 GAGAGTGAAGTACCTGA-AGAGAAAGGCTGCTTTTACTACACCAATTTTACTGTTTC 675
      715 NNAGTWNNNNNNNNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNA 774
      676 TTCTGATTCATTAATCTCTGTTGATTAAGTTCGTGAAGAAACAGCTGTGTTATAGA 735
      775 GAYTKTTTNNNNNTYRGVNTNTAARDGMANNNNNNNNNNNNNGWSMDWMTWMAVAYGT 834
      736 AAACAATTTATCTTCATCCACAGGAGAAATTCATTAATGCAATA 786
      835 NNNNNNNNNNAVAMWTKMYTDDDRWRBAVYTNNNNNNNRAVYGAADVA 885

```

```

RESULT 40
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.T., L.A., and B.N. FAE1 promoters
US-09-806-708B-22

```

```

Query Match      5.8%; Score 46; DB 3; Length 1141;
Best Local Similarity 11.9%; Pred. No. 0.061;
Matches 86; Conservative 241; Mismatches 393; Indels 5; Gaps 1;

```

```

Qy      71 TTGTCCAGTCTACTATAAGACATTAAGTACGTAATAAATATATATGACAAATT 130
      1128 TTKTKYKKAANNNNNNNNNGKMDNNRMDATKYSATGTAMWTHAKRGATWCVYWTGTR 1069
      131 GTGTATTAGATCTGTGGCTAGCAAGAAATTTTCCAGCTGACCTTAACCGAGCC 190
      1068 RWCMTRYAARTWYTRBNANMASCATKEMWMTMKYATKRYRAWYAMMCARNNNMGCATNG 1009
      191 CATCTTGGTATGTTTCAACTATTTGTACATCACTTGAGAGAGTTCAAACTAAG 250
      1008 YAKSCATNNAMWATTRMAAYAAAKARAVAGNNMRYGAAGNKMGCMAMATMGBMWAD 949
      251 AATGATGAGGGAAGAGTGAAGCTGAAGATTAAGTCCACCATTTGACTGATG 310
      948 TKGKMCNNNNNNNTTDRRAAMAKNNNNNNNAATWYACVNPDAATNNKATHTMKWTHGAHS 889
      311 TCAAAAGGCAATTATGCTCTGAATTTTGATGAGGACATTAACCTTTAGCCCATGTTA 370

```

```

Db      888 KATRHHTTRCRRTKXNNNNNNNAATYVYWHABRBMENAMWTRTNNNNNNNNNNACNTR 829
      371 ACATTTCTTCAGAGATTCATTAATTAATTAATTAAGAAAAGTTTTCCTGGAT 430
      828 TWAABWACSCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 769
      431 CATTAACATCAGAAATATAGAAATGAATGCCACATGAAATATCAAAAGAAATTA 490
      768 AVTTHTDWCYKTWATWTDWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 709
      491 AATCATTAAGACACAAACATATGATATTTGTCATCTGCTCTTAAGCAATGTTATG 550
      708 KAYVAATNNWG-----CMNNNTDARTNNNTYMRBRMWTNTKRYSTRRHHYGTATN 654
      551 TTAATTTCTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTACTAGTTATG 610
      653 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 594
      611 ATTCAGGAGAGTACTCTGATGAAGAGAGCTGCTTTTACTACACCATTTTATGTC 670
      593 WYANMRCSDVYTRNNNTYCKSYASHYWYSSNNAWYRYSARWSSMARWTRNNMWS 534
      671 TTTCTTCTGAATTCATTAATCTCTGTTGATTAAGTTCGTGAAGAAACAGCTGTAT 730
      533 GBVRMNACTMWRBHHNNNNNTDRIYWWYKRAABETTYVDSNCAMKSMRGNNMRAM 474
      731 ATGAAAACAAATTTATCTTCATCCACAGGAGAAATTCATTAATGCAATAATTA 790
      473 WNAANNDAAGAMHTWYWMGNNTWMMRBAWKNMAMACBRAYCCNNNNNNACVHKKMNR 414
      791 CGTT 795
      413 WTKY 409

```

```

RESULT 41
US-09-949-016-13276
; Sequence 13276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13276
; LENGTH: 100877
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)..(100877)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13276

```

```

Query Match      5.8%; Score 46; DB 3; Length 100877;
Best Local Similarity 54.0%; Pred. No. 0.2;
Matches 94; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

```

```

Qy      389 ATTACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 448
      14071 AATACTTTTAAATGTTTATTTTAAACAATTTTACATGAGAAAATATCTTTCTACAT 14130

```

```

Query Match      5.6%; Score 44.6; DB 3; Length 832;
Best Local Similarity 17.7%; Pred. No. 0.13;
Matches 59; Conservative 125; Mismatches 149; Indels 0; Gaps 0;

Oy      462  A C A C T G A T A T C A A A A G A A A A A A A C T A A A A C A T T A T T A A G A C A C A C C A T G T G A T A T T      521
Db      431  A C T T G A C T A T G A A C T A A C C A G A T T T G C T A A A G T C A A G A A T T G T A C C A T A A T A A T A T T      372

Oy      522  T G T C A C T C T G C T T T A A G A A A G T T A T G T A T T A T T C T T G C A A C C C T A C A C A A G G C C A      581
Db      371  A T A T T T G T Y T W M W K M T W M T T Y T W T R M W M M K K A R M Y M M K S T Y A C A S R Y K Y T W G W      312

Oy      582  G A A A T T A C A C A G A T A C T A G T T A T T G G T T A T T C A C G A G A G A G A G A C T G A A G A G A G      641
Db      311  W W W M M R M M S T R Y C Y W C M K C M C Y R R G R C A W Y M A G R M M S Y A M G K M S R M S A M S C T R M      252

Oy      642  G C T G T C C T T T A C T A C A C C A T T T T A G T C T T T C T T C T T G A A T T C A T T A C T T C C T T G A      701
Db      251  Y Y K G S Y T W M K C T C A T W C Y W K M K R M M S K T C W S G R G Y M T S Y T S R S Y S M Y A M S M      192

Oy      702  T A A G T T C T G T A A A A A C A G C T G T A T T A T T A T A G A A A A C A A T T A T T C C T A T C C A C A G      761
Db      191  Y T M C M M G R M W S T Y W Y A M G K M M R Y A T T R R L A M M M A A M T M M Y M W A M C M S S R G A A M      132

Oy      762  G A A A T T C A T T A C T T A A T G C C A A T A A T T A C G T T      794
Db      131  Y R R T M M M G Y R W M R K K S Y R R T C A M A Y A M K T K      99

RESULT 44
US-09-130-616-168/C
; Sequence 168, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monla, Brecht
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 168
US-09-130-616-168
; LENGTH: 1349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-168

Query Match      5.5%; Score 44.4; DB 3; Length 1349;
Best Local Similarity 69.8%; Pred. No. 0.16;
Matches 60; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy      626  G T A C C T G A A G A G A A A G G C T G T C C T T T A C T A C A C A T T T T A A G T C T T T C T T C G A A T T C      685
Db      1155  G C A C C T A A A A G A A G A G G C T G C C C C C G T A A T A C C A T T C T T G T T C T C T C C A A G T C      1096

Oy      686  A T T A C T T C C T T G A G A T A A G T T C T G T      711
Db      1095  A T A A C T T C C T T A T A T A C A T T C T T T      1070

RESULT 45
US-09-130-616-166/C
; Sequence 166, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.

```



```
RESULT 48
US-09-130-616-167/C
; Sequence 167, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 167
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-167

Query Match
Best Local Similarity 5.2%; Score 42; DB 3; Length 1311;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGAATTCATTA 689
DB 1156 CTAAAGAGAGGGCTGCCCCCGTATATCAATCTTGTTCTCTCCCAAGTCATTA 1097
QY 690 CTCTCTGTAGATAGTTCTGT 711
DB 1096 CTTCCTTATATATCAATCTTT 1075

RESULT 49
US-09-209-668-14/C
; Sequence 14, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0316
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1173)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L26318/Genbank
; DATABASE ENTRY DATE: 1994-04-25
US-09-209-668-14

Query Match
Best Local Similarity 5.2%; Score 42; DB 3; Length 1418;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGAATTCATTA 689
DB 1156 CTAAAGAGAGGGCTGCCCCCGTATATCAATCTTGTTCTCTCCCAAGTCATTA 1097
```

```
QY 690 CTTCCTGTAGATAGTTCTGT 711
DB 1096 CTTCCTTATATATCAATCTTT 1075

RESULT 50
US-09-130-616-164/C
; Sequence 164, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 164
; LENGTH: 1418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-616-164

Query Match
Best Local Similarity 5.2%; Score 42; DB 3; Length 1418;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTGCTTTCTTCTGAATTCATTA 689
DB 1156 CTAAAGAGAGGGCTGCCCCCGTATATCAATCTTGTTCTCTCCCAAGTCATTA 1097
QY 690 CTTCCTGTAGATAGTTCTGT 711
DB 1096 CTTCCTTATATATCAATCTTT 1075

Search completed: July 19, 2006, 20:14:12
Job time : 207 secs
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 19:12:50 ; Search time 1474 Seconds
(without alignments)
6669.002 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800
Sequence: 1 acattttccaaaccttca.....caataatcagcttgatgc 800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA Main:

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq.*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798.4	99.8	76500	10 US-10-723-681-2	Sequence 2, Appli
2	798.4	99.8	110950	10 US-10-857-780-2	Sequence 2, Appli
3	796.8	99.6	2669	4 US-09-925-065A-663710	Sequence 683710,
4	796.8	99.6	2669	4 US-09-925-065A-663711	Sequence 683711,
5	796.8	99.6	2669	4 US-09-925-065A-663712	Sequence 683712,
6	796.8	99.6	2669	5 US-09-925-065A-663710	Sequence 683710,
7	796.8	99.6	2669	5 US-09-925-065A-663711	Sequence 683711,
8	796.8	99.6	2669	5 US-09-925-065A-663712	Sequence 683712,
9	463.4	57.9	823	10 US-10-857-780-4942	Sequence 4942, Ap
10	463.4	57.9	823	10 US-10-857-780-4943	Sequence 4943, Ap
11	456.4	57.0	572	5 US-09-925-065A-44644	Sequence 44644, A
12	456.4	57.0	572	5 US-09-925-065A-44644	Sequence 44644, A
13	456.4	57.0	572	12 US-10-301-480-145882	Sequence 145882,
14	456.4	57.0	572	12 US-10-301-480-145882	Sequence 145882,
15	82.8	10.3	1422	3 US-09-909-650A-23	Sequence 23, Appli
16	82.8	10.3	1505	3 US-09-165-522-1	Sequence 1, Appli
17	82.8	10.3	1505	8 US-10-641-643-952	Sequence 952, App

18	82.8	10.3	1505	8 US-10-343-710-56	Sequence 56, Appli
19	82.8	10.3	1505	16 US-11-180-044-1	Sequence 1, Appli
20	82.8	10.3	2211	15 US-11-127-817-10	Sequence 10, Appli
21	82.8	10.3	2367	3 US-09-165-522-3	Sequence 3, Appli
22	82.8	10.3	2367	16 US-11-180-044-3	Sequence 3, Appli
23	82.8	10.3	2677	10 US-10-765-700-34	Sequence 34, Appli
24	82.8	10.3	2698	15 US-11-127-817-11	Sequence 11, Appli
25	80.4	10.1	922	10 US-10-450-763-29386	Sequence 29386, A
26	80.4	10.1	999	10 US-10-450-763-2768	Sequence 2768, Ap
27	80.4	10.1	1111	10 US-10-450-763-11488	Sequence 11488, A
28	80.4	10.1	1306	3 US-09-909-650A-22	Sequence 22, Appli
29	80.4	10.1	1773	3 US-09-165-522-4	Sequence 4, Appli
30	80.4	10.1	1773	8 US-10-343-710-54	Sequence 54, Appli
31	80.4	10.1	1773	16 US-11-180-044-4	Sequence 4, Appli
32	80.4	10.1	1872	10 US-10-450-763-19249	Sequence 19249, A
33	80.4	10.1	2131	3 US-09-771-161A-87	Sequence 87, Appli
34	80.4	10.1	2155	15 US-11-127-817-12	Sequence 12, Appli
35	80.4	10.1	2372	3 US-09-165-522-6	Sequence 6, Appli
36	80.4	10.1	2372	3 US-09-165-522-7	Sequence 7, Appli
37	80.4	10.1	2372	7 US-10-305-720-1389	Sequence 1389, Ap
38	80.4	10.1	2372	10 US-10-466-162-5	Sequence 5, Appli
39	80.4	10.1	2372	10 US-10-723-681-9	Sequence 9, Appli
40	80.4	10.1	2372	10 US-10-857-780-11	Sequence 11, Appli
41	80.4	10.1	2372	15 US-11-127-817-9	Sequence 9, Appli
42	80.4	10.1	2372	16 US-11-180-044-6	Sequence 6, Appli
43	80.4	10.1	2372	16 US-11-180-044-7	Sequence 7, Appli
44	80.4	10.1	2382	10 US-10-765-700-33	Sequence 33, Appli
45	80.4	10.1	8750	3 US-09-776-167A-8	Sequence 8, Appli
46	66.8	8.3	1975	16 US-11-136-527-4334	Sequence 4334, Ap
47	66.8	8.3	1975	8 US-09-165-522-9	Sequence 9, Appli
48	66.8	8.3	1975	8 US-10-343-710-60	Sequence 60, Appli
49	66.8	8.3	1975	16 US-11-180-044-9	Sequence 9, Appli
50	66.8	8.3	1975	16 US-11-180-044-9	Sequence 9, Appli
51	66.8	8.3	1975	16 US-11-136-527-238	Sequence 238, App
52	64.4	8.1	2322	8 US-10-343-710-58	Sequence 58, Appli
53	64.4	8.1	2322	16 US-11-180-044-11	Sequence 11, Appli
54	50.8	6.3	600	16 US-11-136-527-4293	Sequence 4293, Ap
55	50.8	6.3	1408	16 US-11-136-527-197	Sequence 197, App
56	49.4	6.2	520	8 US-10-404-460-104	Sequence 104, App
57	49.2	6.2	520	4 US-09-925-065A-357307	Sequence 357307,
58	49.2	6.2	520	5 US-09-925-065A-357307	Sequence 357307,
59	49.2	6.2	535	12 US-10-301-480-128623	Sequence 128623,
60	49.2	6.2	535	12 US-10-301-480-1042032	Sequence 1042032,
61	48.8	6.1	2372	7 US-10-104-041-1930	Sequence 1930, Ap
62	48.8	6.1	2372	16 US-11-072-512-1930	Sequence 21042, A
63	48.4	6.0	450	8 US-10-242-532A-21042	Sequence 21042, A
64	48.4	6.0	450	8 US-10-085-783A-21042	Sequence 3619, Ap
65	48.4	6.0	600	13 US-11-060-756-3619	Sequence 3620, Ap
66	48.4	6.0	600	13 US-11-060-756-3620	Sequence 7891, Ap
67	48.4	6.0	600	13 US-11-060-756-7891	Sequence 7892, Ap
68	48.4	6.0	1780	3 US-09-861-097-17	Sequence 17, Appli
69	48.4	6.0	1780	3 US-09-861-098-17	Sequence 17, Appli
70	48.4	6.0	1780	3 US-09-861-012-17	Sequence 17, Appli
71	48.4	6.0	1780	10 US-10-972-052-17	Sequence 17, Appli
72	48.4	6.0	1780	7 US-10-204-041-11	Sequence 11, Appli
73	48.4	6.0	1782	8 US-10-345-444B-167	Sequence 167, App
74	48.4	6.0	1930	13 US-11-019-829-74	Sequence 74, Appli
75	48.4	6.0	1930	13 US-11-019-829-74	Sequence 77, Appli
76	48.4	6.0	36000	10 US-10-948-974A-27	Sequence 27, Appli
77	48.4	6.0	520	4 US-09-925-065A-357306	Sequence 357306,
78	48.4	6.0	520	4 US-09-925-065A-357308	Sequence 357308,
79	48.4	6.0	520	5 US-09-925-065A-357306	Sequence 357306,
80	48.4	6.0	520	5 US-09-925-065A-357308	Sequence 357308,
81	48.4	6.0	520	5 US-09-925-065A-357308	Sequence 357308,
82	48.4	6.0	535	12 US-10-301-480-128622	Sequence 428622,
83	48.4	6.0	535	12 US-10-301-480-128624	Sequence 428624,
84	48.4	6.0	535	12 US-10-301-480-1042031	Sequence 1042031,
85	48.4	6.0	535	12 US-10-301-480-1042033	Sequence 1042033,
86	46.8	5.8	1392	8 US-10-641-643-953	Sequence 953, App
87	46.8	5.8	1392	10 US-10-466-162-8	Sequence 9, Appli
88	46.8	5.8	1873	3 US-09-954-531-15	Sequence 15, Appli
89	46.8	5.8	1873	7 US-10-305-770-1437	Sequence 1437, Ap
90	46.8	5.8	1873	10 US-10-843-641A-1222	Sequence 1222, Ap

C 91	46.8	5.8	1973	10	US-10-0782-445-12	Sequence 12, Appl
C 92	46.8	5.8	1940	13	US-11-019-829-75	Sequence 75, Appl
C 93	46.8	5.8	1940	13	US-11-019-829-75	Sequence 76, Appl
C 94	46.6	5.7	1940	4	US-09-922-065A-758673	Sequence 758673,
C 95	45.6	5.7	4004	4	US-09-923-065A-758673	Sequence 758673,
C 96	45.6	5.7	5986	8	US-10-1221-613-396	Sequence 336, Appl
C 97	44.4	5.5	4004	4	US-09-923-065A-758672	Sequence 758672,
C 98	44.4	5.5	4004	5	US-09-923-065A-758672	Sequence 758672,
C 99	44.4	5.5	600	13	US-11-060-756-176	Sequence 376, Appl
C 100	44.4	5.5	600	13	US-11-060-756-177	Sequence 377, Appl

ALIGNMENTS

```

RESULT 1
US-10-723-681-2
Sequence 2, Application US/10723681
Publication No. US2005019223A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: RENEHLAND, RIKARD
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND
TITLE OF INVENTION: TREATMENTS THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/723,681
CURRENT FILING DATE: 2003-11-25
PRIORITY APPLICATION NUMBER: US 60/429,136
PRIORITY FILING DATE: 2002-11-25
PRIORITY APPLICATION NUMBER: US 60/490,234
PRIORITY FILING DATE: 2003-07-24
NUMBER OF SEQ ID NOS: 835
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 76500
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-681-2

```

[illegible]

Qy	421	TGTCCTGGATCATTTACATCAGATATATAGAAATGACCACTGAATATCAAAAGAA	480
Dd	36621	TGTCCTGGATCATTTACATCAGATATATAGAAATGATCCCACTGAATATCAAAAGAA	36480
Qy	481	ATAAAACTAAATCATTTATPAAGACAAACATGTGATATTTTGTCATCTGCTTTAAG	540
Dd	36481	ATAAAACTAAATCATTTATPAAGACAAACATGTGATATTTTGTCATCTGCTTTAAG	36540
Qy	541	CAATGTTATGTTATTTCTTGCAACCCCTACAAAGGCCAABAATTCACAAAGTACTAG	600
Dd	36541	CAATGTTATGTTATTTCTTGCAACCCCTACAAAGGCCAABAATTCACAAAGTACTAG	36600
Qy	601	TTTATTGGTTATTCACGAGAGTGAATCCTGAAGAGAGAGGCTGCTTTACTACACC	660
Dd	36601	TTTATTGGTTATTCACGAGAGTGAATCCTGAAGAGAGAGGCTGCTTTACTACACC	36660
Qy	661	ATTTTATGCTTTTCTTCTGAAATCTTACTTCTTTGATGATAGTCTGTGAGAAACAG	720
Dd	36661	ATTTTATGCTTTTCTTCTGAAATCTTACTTCTTTGATGATAGTCTGTGAGAAACAG	36720
Qy	721	CTGTGTTATTTATGAAACAAATTTATCTTATCATCCACAGGGAATTCATTAATGAC	780
Dd	36721	CTGTGTTATTTATGAAACAAATTTATCTTATCATCCACAGGGAATTCATTAATGAC	36780
Qy	781	CAATATATTAACGTTTGTAGT 800	
Dd	36781	CAATATATTAACGTTTGTAGT 36800	

```

RESULT 2
US-10-857-780-2
; Sequence 2, Application US/10857780
; Publication No. US20050272043A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
FILE REFERENCE: SEO-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 110950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-857-780-2

Query Match          99.8%; Score 798.4; DB 10; Length 110950;
Best Local Similarity 99.9%; Pred. No. 2,6e-178;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ACATTTTCTAAAACTCTTTATAGTGAAGACATAGGCTCTTAGGAAAAAATATATTGACATT 60
DB      36016 ACATTTTCTAAAACTCTTTATAGTGAAGACATAGGCTCTTAGGAAAAAATATATTGACATT 36075

QY      61 AATAATAAATTTGTCTCAAGTCATCTACTAAGACATTTCTAGAGATCAGTAAAAAATATAT 120
DB      36076 AATAATAAATTTGTCTCAAGTCATCTACTAAGACATTTCTAGAGATCAGTAAAAAATATAT 36135

QY      121 ATGCACAAATGTGTATTAAGATCTCTGTGGCTAGCAAAACGAAAAATTTTCCAAAGCTGACCTT 180

```

```
Db 36136 ATGACAAATTGTGATTAGATTCTGTGCTAGCAAGAAAGAAAATTTTCCAAAGCTGACCTT 36195
QY 181 AACCGGAGCCCATTTGGTAGATGTTTCAACTATTTGCACATCAACCTTGAGAAAGATTC 240
Db 36196 AACCGGAGCCCATTTGGTAGATGTTTCAACTATTTGCACATCAACCTTGAGAAAGATTC 36255
QY 241 AAACACTAAGAAATGAGGAGAGAGTAGCGGCTGAAAGAGATTACTGAGCTCCACATT 300
Db 36256 AAACACTAAGAAATGAGGAGAGAGTAGCGGCTGAAAGAGATTACTGAGCTCCACATT 36315
QY 301 GACTTGATGCTCAAAAGGCAATTATGCTCTGCAATTTTGATGAGGCACTTAAACCTTTA 360
Db 36316 GACTTGATGCTCAAAAGGCAATTATGCTCTGCAATTTTGATGAGGCACTTAAACCTTTA 36375
QY 361 GCCCATGTTAACTTTTCTTCAGGATTCATTACTATTAAATTTATTTATGAAAAAGTTT 420
Db 36376 GCCCATGTTAACTTTTCTTCAGGATTCATTACTATTAAATTTATTTATGAAAAAGTTT 36435
QY 421 TGTCTGGATCATTAACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAGAA 480
Db 36436 TGTCTGGATCATTAACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAGAA 36495
QY 481 ATAAACTAAATCATTTATAGACACAAACCATGATATTTTGCCATCTGCTCTTTAG 540
Db 36496 ATAAACTAAATCATTTATAGACACAAACCATGATATTTTGCCATCTGCTCTTTAG 36555
QY 541 CAATGTTATGTTATTTCTTGCACACCCCTACACAAAGGCCAAGAAATTCACAAGTACTAG 600
Db 36556 CAATGTTATGTTATTTCTTGCACACCCCTACACAAAGGCCAAGAAATTCACAAGTACTAG 36615
QY 601 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGGCTGCTCTTTTCTACAC 660
Db 36616 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGGCTGCTCTTTTCTACAC 36675
QY 661 ATTTTAGTCTTTTCTTCTGAAATTCATCTCTCTTGATGATTAAGTTCTGTAAGAAACAG 720
Db 36676 ATTTTAGTCTTTTCTTCTGAAATTCATCTCTCTTGATGATTAAGTTCTGTAAGAAACAG 36735
QY 721 CTGTGTTATTTATGAAAACAAAATTTATCTTCATCCACAGGGAATTCATTACTTAATGC 780
Db 36736 CTGTGTTATTTATGAAAACAAAATTTATCTTCATCCACAGGGAATTCATTACTTAATGC 36795
QY 781 CAATTAATTACGTTTGATG 800
Db 36796 CAATTAATTACGTTTGATG 36815

RESULT 3
US-09-925-065A-683710/c
; Sequence 683710, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683710
; LENGTH: 2669
```

```
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-683710
Query Match 99.6%; Score 796.8; DB 4; Length 2669;
Best Local Similarity 99.8%; Pred. No. 1,2e-178;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACATTTTCTAAAACCTTTTATAGTAGAGCATGATGCTTTAGAGAAAAATATATATAGCATT 60
Db 1478 ACATTTTCTAAAACCTTTTATAGTAGAGCATGATGCTTTAGAGAAAAATATATATAGCATT 1419
QY 61 AATAAGTAATGTCTCAAGTCACTATAAGCACTTACTAGAGTCAATTAATATATATATATATAT 120
Db 1418 AATAAGTAATGTCTCAAGTCACTATAAGCACTTACTAGAGTCAATTAATATATATATATATAT 1359
QY 121 ATGCACAATGTGTATTAATGATTCGTGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 180
Db 1358 ATGCACAATGTGTATTAATGATTCGTGCTAGCAAAAGAAAAATTTTCCAGCTGACCTT 1299
QY 181 AACCGGAGCCCATCTTGTAGATGTTTCACTATTGTCACTACCTTGAAGAGATTC 240
Db 1298 AACCGGAGCCCATCTTGTAGATGTTTCACTATTGTCACTACCTTGAAGAGATTC 1239
QY 241 AAACACTAAGAAATGAGGAGAGTAGCGGCTGAAAGAGATTAAGTCACTCCACATT 300
Db 1238 AAACACTAAGAAATGAGGAGAGTAGCGGCTGAAAGAGATTAAGTCACTCCACATT 1179
QY 301 GACTTGATGCTCAAAAGGCACTTATGCTCTGAAATTTTGATGAGGCACTTAAACCTTTA 360
Db 1178 GACTTGATGCTCAAAAGGCACTTATGCTCTGAAATTTTGATGAGGCACTTAAACCTTTA 1119
QY 361 GCCCATGTTAACTTTTCTTCTGAAATTCATCTCTCTTGATGATTAAGTTCTGTAAGAAACAG 420
Db 1118 GCCCATGTTAACTTTTCTTCTGAAATTCATCTCTCTTGATGATTAAGTTCTGTAAGAAACAG 1059
QY 421 TGTCTGGATCATTAACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAGAAAG 480
Db 1058 TGTCTGGATCATTAACATGAGAAATATGCAATGAAATGCGACACTGAAATATCAAGAAAG 999
QY 481 ATAAACTAAATCATTTATAGACACAAACCATGATATTTTGCCATCTGCTCTTTAG 540
Db 998 ATAAACTAAATCATTTATAGACACAAACCATGATATTTTGCCATCTGCTCTTTAG 939
QY 541 CAATGTTATGTTATTTCTTGCACACCCCTACACAAAGGCCAAGAAATTCACAAGTACTAG 600
Db 938 CAATGTTATGTTATTTCTTGCACACCCCTACACAAAGGCCAAGAAATTCACAAGTACTAG 879
QY 601 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGGCTGCTTTACTACAC 660
Db 878 TTATATGTTATTCAGGAGAGTAGAGTACTGAAAGAGAGGCTGCTTTACTACAC 819
QY 661 ATTTTAGTCTTTTCTTCTGAAATTCATCTCTCTTGATGATTAAGTTCTGTAAGAAACAG 720
Db 818 ATTTTAGTCTTTTCTTCTGAAATTCATCTCTCTTGATGATTAAGTTCTGTAAGAAACAG 759
QY 721 CTGTGTTATTTATGAAAACAAAATTTATCTTCATCCACAGGGAATTCATTACTTAATGC 780
Db 758 CTGTGTTATTTATGAAAACAAAATTTATCTTCATCCACAGGGAATTCATTACTTAATGC 699
QY 781 CAATTAATTACGTTTGATG 800
Db 698 CAATTAATTACGTTTGATG 679

RESULT 4
US-09-925-065A-683711/c
; Sequence 683711, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 683711
LENGTH: 2669
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-683711
```

Query Match 99.6%; Score 796.8; DB 4; Length 2669;

Best Local Similarity 99.8%; Pred. No. 1.2e-178;

Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ACATTTCTAAACCTTTATAGTGAAGCATGCTTGAAGAAAATATATAGCATT 60
DB 1478 ACATTTCTAAACCTTTATAGTGAAGCATGCTTGAAGAAAATATATAGCATT 1419
QY 61 AATAGTAATGTCTCAAGTCTACTAAAGCATTAAGATGATGATTAATATATAT 120
DB 1418 AATAGTAATGTCTCAAGTCTACTAAAGCATTAAGATGATGATTAATATATAT 1359
QY 121 ATGCAAAATGTGTATTAATCTGTGCTAGCAAAAGAAAATTTCCAGCTGACT 180
DB 1358 ATGCAAAATGTGTATTAATCTGTGCTAGCAAAAGAAAATTTCCAGCTGACT 1299
QY 181 AACCGAGCCCATCTTGTGATGATGTTCACTATTGTCTCACTAACCTTGAGAGTTC 240
DB 1298 AACCGAGCCCATCTTGTGATGATGTTCACTATTGTCTCACTAACCTTGAGAGTTC 1239
QY 241 AAACCTAAGATGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 1238 AAACCTAAGATGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1179
QY 301 GACTTGATGATCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 1178 GACTTGATGATCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1119
QY 361 GCCCATGTTAACTTTCTTCAGAGTTCATTAATTAATTAATTAATTAATTAATTA 420
DB 1118 GCCCATGTTAACTTTCTTCAGAGTTCATTAATTAATTAATTAATTAATTAATTA 1059
QY 421 TGTCCGATGATCAATTAACATCAGAAATATGAAATGAAATGAAATGAAATGAA 480
DB 1058 TGTCCGATGATCAATTAACATCAGAAATATGAAATGAAATGAAATGAAATGAA 999
QY 481 ATAAAACTAAATCATTAATGAGACAAACATGATATTTGTCCATGTGCTTTAAG 540
DB 998 ATAAAACTAAATCATTAATGAGACAAACATGATATTTGTCCATGTGCTTTAAG 939
QY 541 CAATGTATGTTATTTCTTCGAAACCCCTTACAAAGGAGGAGGAGGAGGAGGAGG 600
DB 938 CAATGTATGTTATTTCTTCGAAACCCCTTACAAAGGAGGAGGAGGAGGAGGAGG 879
QY 601 TTTATGTTATTAACGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
DB 878 TTTATGTTATTAACGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 819
QY 661 ATTTTATGTTCTTTCTTCGAAATTCATTTCTTTGAGATGATTTCTGTAAGAAAC 720
DB 818 ATTTTATGTTCTTTCTTCGAAATTCATTTCTTTGAGATGATTTCTGTAAGAAAC 759
```

```
QY 721 CTGTGTATTAATGAGAAACAAATTAATCTTCATCCACAGGGAATTAATTAATGC 780
DB 758 CTGTGTATTAATGAGAAACAAATTAATCTTCATCCACAGGGAATTAATTAATGC 699
QY 781 CAATTAATTAAGTTTGTGATG 800
DB 698 CAATTAATTAAGTTTGTGATG 679
```

RESULT 5
US-09-925-065A-683712/c

Sequence 683712, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925, 065A

SEQUENCE ID NO: 683712

SOFTWARE: FastSeq for Windows Version 4.0

SEQUENCE ID NO: 683712

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-683712

Query Match 99.6%; Score 796.8; DB 4; Length 2669;
Best Local Similarity 99.8%; Pred. No. 1.2e-178;
Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ACATTTCTAAACCTTTATAGTGAAGCATGCTTGAAGAAAATATATAGCATT 60
DB 1478 ACATTTCTAAACCTTTATAGTGAAGCATGCTTGAAGAAAATATATAGCATT 1419
QY 61 AATAGTAATGTCTCAAGTCTACTAAAGCATTAAGATGATGATTAATATATATAT 120
DB 1418 AATAGTAATGTCTCAAGTCTACTAAAGCATTAAGATGATGATTAATATATATAT 1359
QY 121 ATGCAAAATGTGTATTAATCTGTGCTAGCAAAAGAAAATTTCCAGCTGACT 180
DB 1358 ATGCAAAATGTGTATTAATCTGTGCTAGCAAAAGAAAATTTCCAGCTGACT 1299
QY 181 AACCGAGCCCATCTTGTGATGATGTTCACTATTGTCTCACTAACCTTGAGAGTTC 240
DB 1298 AACCGAGCCCATCTTGTGATGATGTTCACTATTGTCTCACTAACCTTGAGAGTTC 1239
QY 241 AAACCTAAGATGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 1238 AAACCTAAGATGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1179
QY 301 GACTTGATGATCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 1178 GACTTGATGATCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1119
QY 361 GCCCATGTTAACTTTCTTCAGAGTTCATTAATTAATTAATTAATTAATTAATTA 420
DB 1118 GCCCATGTTAACTTTCTTCAGAGTTCATTAATTAATTAATTAATTAATTAATTA 1059
QY 421 TGTCCGATGATCAATTAACATCAGAAATATGAAATGAAATGAAATGAAATGAA 480
DB 1058 TGTCCGATGATCAATTAACATCAGAAATATGAAATGAAATGAAATGAAATGAA 999
```

QY 481 ATAAACTAAATCATTATTAAGACACACACCATGTGATATTTGTCATCTCTTTAG 540
 Db 998 ATAAACTAAATCATTATTAAGACACACACCATGTGATATTTGTCATCTCTTTAG 939
 QY 541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACACAGTACTAG 600
 Db 938 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACACAGTACTAG 879
 QY 601 TTTATGTTATTAACCGAGAGTACGTAACCTGAAAGGAGGAGGCTGCTTTTACTACACC 660
 Db 878 TTTATGTTATTAACCGAGAGTACGTAACCTGAAAGGAGGAGGCTGCTTTTACTACACC 819
 QY 661 ATTTTAGCTTTTCTTCTGCAATTCATTAATCTGTTAGATTAAGTCTGTAAGAAACAG 720
 Db 818 ATTTTAGCTTTTCTTCTGCAATTCATTAATCTGTTAGATTAAGTCTGTAAGAAACAG 759
 QY 721 CTGTGTTATTAAGAAACAAATTTATCTTCATCCACAGGAAATTCATTAATGTC 780
 Db 758 CTGTGTTATTAAGAAACAAATTTATCTTCATCCACAGGAAATTCATTAATGTC 699
 QY 781 CAATAATTAACGTTTGATG 800
 Db 698 CAATAATTAACGTTTGATG 679

RESULT 6

US-09-925-065A-683710/C
 / Sequence 683710, Application US/09925065A
 / Publication No. US20050228172A9
 / GENERAL INFORMATION:
 / APPLICANT: Wang, David G.
 / TITLE OF INVENTION: Identification and Mapping of Single
 / FILE REFERENCE: 108827.135
 / CURRENT APPLICATION NUMBER: US/09/925,065A
 / PRIOR FILING DATE: 2001-08-08
 / PRIOR APPLICATION NUMBER: US 60/243,096
 / PRIOR FILING DATE: 2000-10-24
 / PRIOR APPLICATION NUMBER: US 60/252,147
 / PRIOR FILING DATE: 2000-11-20
 / PRIOR APPLICATION NUMBER: US 60/250,092
 / PRIOR FILING DATE: 2000-11-30
 / PRIOR APPLICATION NUMBER: US 60/261,766
 / PRIOR FILING DATE: 2001-01-16
 / PRIOR APPLICATION NUMBER: US 60/289,846
 / PRIOR FILING DATE: 2001-05-09
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 683710
 / LENGTH: 2669
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-09-925-065A-683710

Query Match 99.6%; Score 796.8; DB 5; Length 2669;

Best Local Similarity 99.8%; Pred. No. 1.2e-178;

Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACATTTTCTAAACCTTTATAGTAGAGAGCATGCTTTAGAAAAATATATTTACATT 60
 Db 1478 ACATTTTCTAAACCTTTATAGTAGAGAGCATGCTTTAGAAAAATATATTTACATT 1419
 QY 61 AATTAATTAATTTCTCAAGTCTACTAAAGCATTAATGATCAGTAAATAATATAT 120
 Db 1418 AATTAATTAATTTCTCAAGTCTACTAAAGCATTAATGATCAGTAAATAATATAT 1359
 QY 121 ATGCAAAATGTTATTTAGATTTCTGTGGTAGCAAGAAAGAAATTTTCCAGGTGACTT 180
 Db 1358 ATGCAAAATGTTATTTAGATTTCTGTGGTAGCAAGAAAGAAATTTTCCAGGTGACTT 1299
 QY 181 AACCGAGCCCATCTTGATGATGTTTCAACTAATGTCACATCACTTGAGAGAGTTC 240

Db 1298 AACCGAGCCCATCTTGATGATGTTTCAACTAATGTCACATCACTTGAGAGAGTTC 1239
 QY 241 AACACTAAGATGATGAGGAGAGAGTACGGGCTGAAAGATTTACTGCTCCACATT 300
 Db 1238 AACACTAAGATGATGAGGAGAGAGTACGGGCTGAAAGATTTACTGCTCCACATT 1179
 QY 301 GACTGATGGTCAAAAGGCGATTATGCTGTAATTTTGAAGGACATTTACCTTTA 360
 Db 1178 GACTGATGGTCAAAAGGCGATTATGCTGTAATTTTGAAGGACATTTACCTTTA 1119
 QY 361 GCCCATGTTAAACATTTCTTCAGGATTCATTAATTAATTAATTAAGAAAGTTT 420
 Db 1118 GCCCATGTTAAACATTTCTTCAGGATTCATTAATTAATTAATTAAGAAAGTTT 1059
 QY 421 TGTCTCGATCATTTACATCAGAAATATCAGATGAATGCGACACTGAAATATCAAGAA 480
 Db 1058 TGTCTCGATCATTTACATCAGAAATATCAGATGAATGCGACACTGAAATATCAAGAA 999
 QY 481 ATAAACTAAATCATTATTAAGACACACACCATGTGATATTTGTCATCTCTTTAG 540
 Db 998 ATAAACTAAATCATTATTAAGACACACACCATGTGATATTTGTCATCTCTTTAG 939
 QY 541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACACAGTACTAG 600
 Db 938 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACACAGTACTAG 879
 QY 601 TTTATGTTATTAACCGAGAGTACGTAACCTGAAAGGAGGAGGCTGCTTTTACTACACC 660
 Db 878 TTTATGTTATTAACCGAGAGTACGTAACCTGAAAGGAGGAGGCTGCTTTTACTACACC 819
 QY 661 ATTTTAGCTTTTCTTCTGCAATTCATTAATCTGTTAGATTAAGTCTGTAAGAAACAG 720
 Db 818 ATTTTAGCTTTTCTTCTGCAATTCATTAATCTGTTAGATTAAGTCTGTAAGAAACAG 759
 QY 721 CTGTGTTATTAAGAAACAAATTTATCTTCATCCACAGGAAATTCATTAATGTC 780
 Db 758 CTGTGTTATTAAGAAACAAATTTATCTTCATCCACAGGAAATTCATTAATGTC 699
 QY 781 CAATAATTAACGTTTGATG 800
 Db 698 CAATAATTAACGTTTGATG 679

RESULT 7

US-09-925-065A-683711/C
 / Sequence 683711, Application US/09925065A
 / Publication No. US20050228172A9
 / GENERAL INFORMATION:
 / APPLICANT: Wang, David G.
 / TITLE OF INVENTION: Identification and Mapping of Single
 / FILE REFERENCE: 108827.135
 / CURRENT APPLICATION NUMBER: US/09/925,065A
 / PRIOR FILING DATE: 2001-08-08
 / PRIOR APPLICATION NUMBER: US 60/243,096
 / PRIOR FILING DATE: 2000-10-24
 / PRIOR APPLICATION NUMBER: US 60/252,147
 / PRIOR FILING DATE: 2000-11-20
 / PRIOR APPLICATION NUMBER: US 60/250,092
 / PRIOR FILING DATE: 2000-11-30
 / PRIOR APPLICATION NUMBER: US 60/261,766
 / PRIOR FILING DATE: 2001-01-16
 / PRIOR APPLICATION NUMBER: US 60/289,846
 / PRIOR FILING DATE: 2001-05-09
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 683711
 / LENGTH: 2669
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-09-925-065A-683711

Query Match 99.6%; Score 796.8; DB 5; Length 2669;

Best Local Similarity 99.8%; Pred. No. 1.2e-178;
Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACATTTCTTAAACCTTTTATAGTACAGATAGTCTTGAAGAAAATATATAGCATT 60
Db 1478 ACATTTCTTAAACCTTTTATAGTACAGATAGTCTTGAAGAAAATATATAGCATT 1419

QY 61 AATAAGTAATTTGCTCAAGTCATCTAAGCACATTACTAGATCAGTAAAAATATAT 120
Db 1418 AATAAGTAATTTGCTCAAGTCATCTAAGCACATTACTAGATCAGTAAAAATATAT 1359

QY 121 ATGCACATTTGCTATAGATTTCTGTGGCTAGACAAAAGAAAATTTCCAGCTGACCT 180
Db 1358 ATGCACATTTGCTATAGATTTCTGTGGCTAGACAAAAGAAAATTTCCAGCTGACCT 1299

QY 181 AACCGAGCCCATCTGTGATGATGTTCAACTATTTGCATCATCAACCTTGAGAGATTC 240
Db 1298 AACCGAGCCCATCTGTGATGATGTTCAACTATTTGCATCATCAACCTTGAGAGATTC 1239

QY 241 AATCACTAAGATGATGAGGAGAGAGTACGGCTGAAGAGATTACTGAGCTCCACATT 300
Db 1238 AATCACTAAGATGATGAGGAGAGAGTACGGCTGAAGAGATTACTGAGCTCCACATT 1179

QY 301 GACTGATGCTCAAAAGGGCATATGCGCTGCAATTTTGTAGAGCACATTTACCCCTTA 360
Db 1178 GACTGATGCTCAAAAGGGCATATGCGCTGCAATTTTGTAGAGCACATTTACCCCTTA 1119

QY 361 GCCCATGTTAACATTTTCTTCAAGATTCATTACTATTAATTTATGAAAAAGTTT 420
Db 1118 GCCCATGTTAACATTTTCTTCAAGATTCATTACTATTAATTTATGAAAAAGTTT 1059

QY 421 TGCTCGATCATTTACATCAGAAATATCAGATGCAACCTGCAATTTGAAAAAGAA 480
Db 1058 TGCTCGATCATTTACATCAGAAATATCAGATGCAACCTGCAATTTGAAAAAGAA 999

QY 481 APTAACTAAATCATTTATTAAGGACACAAACATGATATTTTGCATCTGCTTTAAG 540
Db 998 APTAACTAAATCATTTATTAAGGACACAAACATGATATTTTGCATCTGCTTTAAG 939

QY 541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTAC 600
Db 938 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTAC 879

QY 601 TTTATGCTTATTCAGGAGAGTGAATCCTGAAGAGAGGCTGCTCTTTACTACAC 660
Db 878 TTTATGCTTATTCAGGAGAGTGAATCCTGAAGAGAGGCTGCTCTTTACTACAC 819

QY 661 ATTTTACGCTTTCTTCTGAAATTCATCTCTGTAGATTAAGTTCTGTAGAAACAG 720
Db 818 ATTTTACGCTTTCTTCTGAAATTCATCTCTGTAGATTAAGTTCTGTAGAAACAG 759

QY 721 CTGTGTTATTAAGAAAACAAATTTATCTTCATCCACAGGAAATTAATTAATGC 780
Db 758 CTGTGTTATTAAGAAAACAAATTTATCTTCATCCACAGGAAATTAATTAATGC 699

QY 781 CAATTAATTAAGCTTTTGATG 800
Db 698 CAATTAATTAAGCTTTTGATG 679

RESULT 8
US-09-925-065A-683712/c
; Sequence 683712, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24

;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 683712
;; LENGTH: 2669
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-683712

Query Match 99.6%; Score 796.8; DB 5; Length 2669;
Best Local Similarity 99.8%; Pred. No. 1.2e-178;
Matches 798; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACATTTCTTAAACCTTTTATAGTACAGATAGTCTTGAAGAAAATATATAGCATT 60
Db 1478 ACATTTCTTAAACCTTTTATAGTACAGATAGTCTTGAAGAAAATATATAGCATT 1419

QY 61 AATAAGTAATTTGCTCAAGTCATCTAAGCACATTACTAGATCAGTAAAAATATAT 120
Db 1418 AATAAGTAATTTGCTCAAGTCATCTAAGCACATTACTAGATCAGTAAAAATATAT 1359

QY 121 ATGCACATTTGCTATAGATTTCTGTGGCTAGACAAAAGAAAATTTCCAGCTGACCT 180
Db 1358 ATGCACATTTGCTATAGATTTCTGTGGCTAGACAAAAGAAAATTTCCAGCTGACCT 1299

QY 181 AACCGAGCCCATCTGTGATGATGTTCAACTATTTGCATCATCAACCTTGAGAGATTC 240
Db 1298 AACCGAGCCCATCTGTGATGATGTTCAACTATTTGCATCATCAACCTTGAGAGATTC 1239

QY 241 AATCACTAAGATGATGAGGAGAGAGTACGGCTGAAGAGATTACTGAGCTCCACATT 300
Db 1238 AATCACTAAGATGATGAGGAGAGAGTACGGCTGAAGAGATTACTGAGCTCCACATT 1179

QY 301 GACTGATGCTCAAAAGGGCATATGCGCTGCAATTTTGTAGAGCACATTTACCCCTTA 360
Db 1178 GACTGATGCTCAAAAGGGCATATGCGCTGCAATTTTGTAGAGCACATTTACCCCTTA 1119

QY 361 GCCCATGTTAACATTTTCTTCAAGATTCATTACTATTAATTTATGAAAAAGTTT 420
Db 1118 GCCCATGTTAACATTTTCTTCAAGATTCATTACTATTAATTTATGAAAAAGTTT 1059

QY 421 TGCTCGATCATTTACATCAGAAATATCAGATGCAACCTGCAATTTGAAAAAGAA 480
Db 1058 TGCTCGATCATTTACATCAGAAATATCAGATGCAACCTGCAATTTGAAAAAGAA 999

QY 481 APTAACTAAATCATTTATTAAGGACACAAACATGATATTTTGCATCTGCTTTAAG 540
Db 998 APTAACTAAATCATTTATTAAGGACACAAACATGATATTTTGCATCTGCTTTAAG 939

QY 541 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTAC 600
Db 938 CAATGTTATGTTATTTCTTGCAACCCCTACACAAAGGCCAAGAAATTAACAAGTAC 879

QY 601 TTTATGCTTATTCAGGAGAGTGAATCCTGAAGAGAGGCTGCTCTTTACTACACC 660
Db 878 TTTATGCTTATTCAGGAGAGTGAATCCTGAAGAGAGGCTGCTCTTTACTACACC 819

QY 661 ATTTTACGCTTTCTTCTGAAATTCATCTCTGTAGATTAAGTTCTGTAGAAACAG 720
Db 818 ATTTTACGCTTTCTTCTGAAATTCATCTCTGTAGATTAAGTTCTGTAGAAACAG 759

QY 721 CTGTGTTATTAAGAAAACAAATTTATCTTCATCCACAGGAAATTAATTAATGC 780
Db 758 CTGTGTTATTAAGAAAACAAATTTATCTTCATCCACAGGAAATTAATTAATGC 699

QY 781 CAATTAATTAAGCTTTTGATG 800

Db 698 CAAATATTAAGTTTATG 679

RESULT 9

US-10-857-780-4942
; Sequence 4942, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: REMELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4942
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-857-780-4942

Query Match 57.9%; Score 463.4; DB 10; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.3e-99;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 336 TTTGATGAGGCACATTTACCCCTTACCCCTGTTAACTTTCTTACAGATTCTATTACTA 395
DB 1 TTTGATGAGGCACATTTACCCCTTACCCCTGTTAACTTTCTTACAGATTCTATTACTA 60
QY 396 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCATCCATGAGATTAATCAGATG 455
DB 61 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCATCCATGAGATTAATCAGATG 120
QY 456 AATGCCACACTGAATATCAAAAGAAATAAATCTAAATCATTTAAGACACACCATGT 515
DB 121 AATGCCACACTGAATATCAAAAGAAATAAATCTAAATCATTTAAGACACACCATGT 180
QY 516 GATATTGTCCATCTGCTCTTTAAGCAATGTATGTTATTTCTGCAACCCCTACACAA 575
DB 181 GATATTGTCCATCTGCTCTTTAAGCAATGTATGTTATTTCTGCAACCCCTACACAA 240
QY 576 GGCAGAAATATACACAAGTACTAGTTTATGTTATTTCTGCAACCCCTACACAA 635
DB 241 GGCAGAAATATACACAAGTACTAGTTTATGTTATTTCTGCAACCCCTACACAA 300
QY 636 GAGAAAGCTGCTCTTTTACTACACATTTTACTCTTTCTTCTGAATTCATTCTCT 695
DB 301 GAGAAAGCTGCTCTTTTACTACACATTTTACTCTTTCTTCTGAATTCATTCTCT 360
QY 696 TGTATTAAGTTCTGTAAAGAAACAGTGTGTATTTAAGAAAACAATTTATCTTCATG 755
DB 361 TGTATTAAGTTCTGTAAAGAAACAGTGTGTATTTAAGAAAACAATTTATCTTCATG 420
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTGTATG 800
DB 421 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTGTATG 465

RESULT 10

US-10-857-780-4943

; Sequence 4943, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: REMELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4943
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-857-780-4943

Query Match 57.9%; Score 463.4; DB 10; Length 823;
Best Local Similarity 99.8%; Pred. No. 1.3e-99;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 336 TTTGATGAGGCACATTTACCCCTTACCCCTGTTAACTTTCTTACAGATTCTATTACTA 395
DB 1 TTTGATGAGGCACATTTACCCCTTACCCCTGTTAACTTTCTTACAGATTCTATTACTA 60
QY 396 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCATCCATGAGATTAATCAGATG 455
DB 61 TTTAAATATTATGAAAAAGTTTGTCTGATCATTCATCCATGAGATTAATCAGATG 120
QY 456 AATGCCACACTGAATATCAAAAGAAATAAATCTAAATCATTTAAGACACACCATGT 515
DB 121 AATGCCACACTGAATATCAAAAGAAATAAATCTAAATCATTTAAGACACACCATGT 180
QY 516 GATATTGTCCATCTGCTCTTTAAGCAATGTATGTTATTTCTGCAACCCCTACACAA 575
DB 181 GATATTGTCCATCTGCTCTTTAAGCAATGTATGTTATTTCTGCAACCCCTACACAA 240
QY 576 GGCAGAAATATACACAAGTACTAGTTTATGTTATTTCTGCAACCCCTACACAA 635
DB 241 GGCAGAAATATACACAAGTACTAGTTTATGTTATTTCTGCAACCCCTACACAA 300
QY 636 GAGAAAGCTGCTCTTTTACTACACATTTTACTCTTTCTTCTGAATTCATTCTCT 695
DB 301 GAGAAAGCTGCTCTTTTACTACACATTTTACTCTTTCTTCTGAATTCATTCTCT 360
QY 696 TGTATTAAGTTCTGTAAAGAAACAGTGTGTATTTAAGAAAACAATTTATCTTCATG 755
DB 361 TGTATTAAGTTCTGTAAAGAAACAGTGTGTATTTAAGAAAACAATTTATCTTCATG 420
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTGTATG 800
DB 421 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTGTATG 465

RESULT 11

US-09-925-065A-44644/c
; Sequence 44644, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome


```
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44644
LENGTH: 572
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-44644

Query Match
Best Local Similarity 57.0%; Score 456.4; DB 4; Length 572;
Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

343 AGGCACATTTACCCCTTTAGCCCATGTTAACATTTCTTCAGATTCTATTAAAT 402
572 AGGCACATTTACCCCTTTAGCCCATGTTAACATTTCTTCAGATTCTATTAAAT 513
403 TATTTATGAAAAAGTTTGTGCTGATCATTAACATTAATGAGATGATGCA 462
512 TATTTATGAAAAAGTTTGTGCTGATCATTAACATTAATGAGATGATGCA 453
463 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATGAGACACACATGTATTT 522
452 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATGAGACACACATGTATTT 393
523 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 582
392 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 333
583 AAATTCACAGTACAGTATTTATGTTATTCAGAGAGTGTCTGGAAGAGAGG 642
332 AAATTCACAGTACAGTATTTATGTTATTCAGAGAGTGTCTGGAAGAGAGG 273
643 CTGTCCTTTACTACACCAATTTAGCTTTCTTCTGAATTCATTACTCTTGAT 702
272 CTGTCCTTTACTACACCAATTTAGCTTTCTTCTGAATTCATTACTCTTGAT 213
703 AAGTTCGTAGAAACAGCTGTATTTATGAAAAAAATTAATTCCTTCATCCAGG 762
212 AAGTTCGTAGAAACAGCTGTATTTATGAAAAAAATTAATTCCTTCATCCAGG 153
763 AAATTCATTACTTAATGCCAAATTAATTAAGTTTGATG 800
152 AAATTCATTACTTAATGCCAAATTAATTAAGTTTGATG 115

RESULT 12
US-09-925-065A-44644/c
Sequence 44644, Application US/09925065A
Publication No. US2005028172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
```

```

PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44644
LENGTH: 572
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-44644

Query Match
Best Local Similarity 57.0%; Score 456.4; DB 5; Length 572;
Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

343 AGGCACATTTACCCCTTTAGCCCATGTTAACATTTCTTCAGATTCTATTAAAT 402
572 AGGCACATTTACCCCTTTAGCCCATGTTAACATTTCTTCAGATTCTATTAAAT 513
403 TATTTATGAAAAAGTTTGTGCTGATCATTAACATTAATGAGATGATGCA 462
512 TATTTATGAAAAAGTTTGTGCTGATCATTAACATTAATGAGATGATGCA 453
463 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATGAGACACACATGTATTT 522
452 CACTGAATATCAAAAGAAATAAATACTAAATCATTAATGAGACACACATGTATTT 393
523 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 582
392 GTTCATCTGCTCTTTAAGCAATGTATTTCTTGCAACCCCTACACAAAGCCAAAG 333
583 AAATTCACAGTACAGTATTTATGTTATTCAGAGAGTGTCTGGAAGAGAGG 642
332 AAATTCACAGTACAGTATTTATGTTATTCAGAGAGTGTCTGGAAGAGAGG 273
643 CTGTCCTTTACTACACCAATTTAGCTTTCTTCTGAATTCATTACTCTTGAT 702
272 CTGTCCTTTACTACACCAATTTAGCTTTCTTCTGAATTCATTACTCTTGAT 213
703 AAGTTCGTAGAAACAGCTGTATTTATGAAAAAAATTAATTCCTTCATCCAGG 762
212 AAGTTCGTAGAAACAGCTGTATTTATGAAAAAAATTAATTCCTTCATCCAGG 153
763 AAATTCATTACTTAATGCCAAATTAATTAAGTTTGATG 800
152 AAATTCATTACTTAATGCCAAATTAATTAAGTTTGATG 115

RESULT 13
US-10-301-480-145882/c
Sequence 145882, Application US/10301480
Publication No. US2006005764A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301, 480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215, 598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311, 695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 145882
LENGTH: 572
TYPE: DNA
ORGANISM: Homo sapiens
US-10-301-480-145882
```

Query Match 57.0%; Score 456.4; DB 12; Length 572;
Best Local Similarity 99.8%; Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 343 AGGCACATTACCTTTAGCCCATGTTTACATTTCTTCAGATTCTTACTATTAAAT 402
DB 572 AGGCACATTACCTTTAGCCCATGTTTACATTTCTTCAGATTCTTACTATTAAAT 513
QY 403 TATTATGAAAAAGTTTGTCTCGATCATTTACATCAGAAATATCAGATGATGCCA 462
DB 512 TATTATGAAAAAGTTTGTCTCGATCATTTACATCAGAAATATCAGATGATGCCA 453
QY 463 CACTGAATATCAAAAGAAATAAATCTAAATCTATTATAGACACAAACCATGATATT 522
DB 452 CACTGAATATCAAAAGAAATAAATCTAAATCTATTATAGACACAAACCATGATATT 393
QY 523 GTTCATCTGCTCTTTAAGCAATGTTATGTTTCTTGCAACCCCTACACAAGGCCAAG 582
DB 392 GTTCATCTGCTCTTTAAGCAATGTTATGTTTCTTGCAACCCCTACACAAGGCCAAG 333
QY 583 AAATTACACAAGTACTAGTTTATGTTTATTCACGAGAGTGAATCTGAAAGAGAAG 642
DB 332 AAATTACACAAGTACTAGTTTATGTTTATTCACGAGAGTGAATCTGAAAGAGAAG 273
QY 643 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGAAATCTTACTCTTGTATGAT 702
DB 272 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGAAATCTTACTCTTGTATGAT 213
QY 703 AAGTCTGTAAAGAAACAGCTGTGTATTTATAGAAAACAATTATCTTCATCCACAGGG 762
DB 212 AAGTCTGTAAAGAAACAGCTGTGTATTTATAGAAAACAATTATCTTCATCCACAGGG 153
QY 763 AAATTCATTACTTAATGCCAAATTAATACGTTTGTATG 800
DB 152 AAATTCATTACTTAATGCCAAATTAATACGTTTGTATG 115

RESULT 14
US-10-301-480-759291/c
; Sequence 759291, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 759291
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-759291

Query Match 57.0%; Score 456.4; DB 12; Length 572;
Best Local Similarity 99.8%; Pred. No. 5.3e-98;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 343 AGGCACATTACCTTTAGCCCATGTTTACATTTCTTCAGATTCTTACTATTAAAT 402
DB 572 AGGCACATTACCTTTAGCCCATGTTTACATTTCTTCAGATTCTTACTATTAAAT 513
QY 403 TATTATGAAAAAGTTTGTCTCGATCATTTACATCAGAAATATCAGAAATGATGCCA 462
DB 512 TATTATGAAAAAGTTTGTCTCGATCATTTACATCAGAAATATCAGAAATGATGCCA 453

QY 463 CACTGAATATCAAAAGAAATAAATCTAAATCTTTATAGACACAAACCATGATATT 522
DB 452 CACTGAATATCAAAAGAAATAAATCTAAATCTTTATAGACACAAACCATGATATT 393
QY 523 GTTCATCTGCTCTTTAAGCAATGTTTATGTTTCTTGCAACCCCTACACAAGGCCAAG 582
DB 392 GTTCATCTGCTCTTTAAGCAATGTTTATGTTTCTTGCAACCCCTACACAAGGCCAAG 333
QY 583 AAATTACACAAGTACTAGTTTATGTTTATTCACGAGAGTGAATCTGAAAGAGAAG 642
DB 332 AAATTACACAAGTACTAGTTTATGTTTATTCACGAGAGTGAATCTGAAAGAGAAG 273
QY 643 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGAAATCTTACTCTTGTATGAT 702
DB 272 CTGTCTTTTACTACACCAATTTTACTCTTTCTTGAAATCTTACTCTTGTATGAT 213
QY 703 AAGTCTGTAAAGAAACAGCTGTGTATTTATAGAAAACAATTATCTTCATCCACAGGG 762
DB 212 AAGTCTGTAAAGAAACAGCTGTGTATTTATAGAAAACAATTATCTTCATCCACAGGG 153
QY 763 AAATTCATTACTTAATGCCAAATTAATACGTTTGTATG 800
DB 152 AAATTCATTACTTAATGCCAAATTAATACGTTTGTATG 115

RESULT 15
US-09-909-650A-23/c
; Sequence 23, Application US/09909650A
; Patent No. US20020165386A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Fournier, Alain
; APPLICANT: Maury, Isabelle
; APPLICANT: Zhou-Liu, Qing
; APPLICANT: Desanlis-Cremont, Francine
; TITLE OF INVENTION: New Polypeptides Derived From JNK3
; FILE REFERENCE: ST99003-US-CNT-1
; CURRENT APPLICATION NUMBER: US/09/909,650A
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/FR00/00104
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/122,175
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 99/00586
; PRIOR FILING DATE: 1999-01-20
; SOFTWARE: Patent In version 3.1
; SEQ ID NO: 23
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-650A-23

Query Match 10.3%; Score 82.8; DB 3; Length 1422;
Best Local Similarity 97.7%; Pred. No. 5.5e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTTTACTACACATTTTATAGCTTTTCTTGAATTC 685
DB 1283 GCACCTGAAGAGAGGCTGCTCTTTTACTACACATTTTATAGCTTTTCTTGAATTC 1224
QY 686 ATTACTTCTCTGTATATAGTTCTGT 711
DB 1223 ATTACTTCTCTGTATATAGTTCTGT 1198

RESULT 16
US-09-165-522-1/c
; Sequence 1, Application US/09165522
; Publication No. US20030023950A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Flavell, Richard A.

Rakic, Pasiko
Whitmarsh, Alan
Kuan, Chia-Yi
Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Faasee, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 68...1459
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-165-522-1
Query Match 10.3%; Score 82.8; DB 3; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5.6e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 1264
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 1263 ATTACTCTCTGTAGATAGTTCTTT 1238
RESULT 17
US-10-641-952/c
Sequence 952, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Jeffrey J. Seilhamer
Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 952:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91463124
SEQUENCE DESCRIPTION: SEQ ID NO: 952 :
US-10-641-643-952
Query Match 10.3%; Score 82.8; DB 8; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5.6e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 1264
QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
DB 1263 ATTACTCTCTGTAGATAGTTCTTT 1238
RESULT 18
US-10-343-710-56/c
Sequence 56, Application US/10343710
Publication No. US20040087478A1
GENERAL INFORMATION:
APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WENNDT, Stephan
APPLICANT: WEIHE, E.
TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 1505
TYPE: DNA
ORGANISM: Homo sapiens
US-10-343-710-56
Query Match 10.3%; Score 82.8; DB 8; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5.6e-09;

Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 1264
QY 686 ATTACTCTCTGTAGATAGTCTGT 711
DB 1263 ATTACTCTCTGTAGATAGTCTTT 1238
RESULT 19
US-11-180-044-1/c
; Sequence 1, Application US/11180044
; Publication No. US2006035303A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Flavell, Richard A.
; APPLICANT: Rakic, Pasko
; APPLICANT: Whitmarsh, Alan
; APPLICANT: Kuan, Chia-Yi
; APPLICANT: Yang, Di
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/180,044
; FILING DATE: 12-JULY-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,522
; FILING DATE: 02-Oct-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,995
; FILING DATE: 03-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 10363/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 68...1459
; US-11-180-044-1
Query Match 10.3%; Score 82.8; DB 16; Length 1505;
Best Local Similarity 97.7%; Pred. No. 5.6e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 1264

QY 686 ATTACTCTCTGTAGATAGTCTGT 711
DB 1263 ATTACTCTCTGTAGATAGTCTTT 1238
RESULT 20
US-11-127-817-10/c
; Sequence 10, Application US/11127817
; Publication No. US20050287519A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koertraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Compositions And Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-D USA
; CURRENT APPLICATION NUMBER: US/11/127,817
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 534
; SOFTWARE: Patencin version 3.3
; SEQ ID NO: 10
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-817-10
Query Match 10.3%; Score 82.8; DB 15; Length 2211;
Best Local Similarity 97.7%; Pred. No. 6.7e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GTACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 685
DB 1323 GCACCTGAAGAGAGGCTGTCTTTACTACACCATTTTACTTTCTTCTGAATTC 1264
QY 686 ATTACTCTCTGTAGATAGTCTGT 711
DB 1263 ATTACTCTCTGTAGATAGTCTTT 1238
RESULT 21
US-09-165-522-3/c
; Sequence 3, Application US/09165522
; Publication No. US20030023990A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Flavell, Richard A.
; APPLICANT: Rakic, Pasko
; APPLICANT: Whitmarsh, Alan
; APPLICANT: Kuan, Chia-Yi
; APPLICANT: Yang, Di
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,522
; FILING DATE: 02-Oct-1998
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-165-522-3

Query Match 10.3%; Score 82.8; DB 3; Length 2367;
Best Local Similarity 97.7%; Pred. No. 6.9e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAATTC 685
DB 1479 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAATTC 1420

QY 686 ATTACTTCTTGTAGATAGTTCTGT 711
DB 1419 ATTACTTCTTGTAGATAGTTCTTT 1394

RESULT 22
US-11-180-044-3/C
Sequence 3, Application US/11180044
Publication No. US20060035303A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Pasako
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-OCT-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2367 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-11-180-044-3

Query Match 10.3%; Score 82.8; DB 16; Length 2367;
Best Local Similarity 97.7%; Pred. No. 6.9e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAATTC 685
DB 1479 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAATTC 1420

QY 686 ATTACTTCTTGTAGATAGTTCTGT 711
DB 1419 ATTACTTCTTGTAGATAGTTCTTT 1394

RESULT 23
US-10-765-700-34/C
Sequence 34, Application US/10765700
Publication No. US20050130171A1
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/10/765,700
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 34
LENGTH: 2677
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 413797.5
FEATURE:
NAME/KEY: unsure
LOCATION: 2024
OTHER INFORMATION: a, t, c, g, or other
US-10-765-700-34

Query Match 10.3%; Score 82.8; DB 10; Length 2677;
Best Local Similarity 97.7%; Pred. No. 7.3e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAATTC 685
DB 1795 GCACCTGAAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAATTC 1736

QY 686 ATTACTTCTTGTAGATAGTTCTGT 711
DB 1735 ATTACTTCTTGTAGATAGTTCTTT 1710

RESULT 24
US-11-127-817-11/C
Sequence 11, Application US/11127817
Publication No. US20050287519A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel

APPLICANT: Splitzele, Koentraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
FILE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27, 800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
LENGTH: 2698
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-817-11

Query Match 10.1%; Score 82.8; DB 15; Length 2698;
Best Local Similarity 97.7%; Pred. No. 7.3e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAGAGAGAGGCTGCTCTTACTACACCATTTTAACTTTCTTCTGAATTC 685
DB 1810 GCACCTGAGAGAGAGGCTGCTCTTACTACACCATTTTAACTTTCTTCTGAATTC 1751
QY 686 ATTACTCTCTGTAGATTAAGTTCTGT 711
DB 1750 ATTACTCTCTGTAGATTAAGTTCTTT 1725

RESULT 25
US-10-450-763-29386/C
Sequence 29386, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 29386
LENGTH: 972
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (373)..(453)
OTHER INFORMATION: 100% homologous to Mus musculus UNK3, accession number
US-10-450-763-29386

Query Match 10.1%; Score 80.4; DB 10; Length 972;
Best Local Similarity 98.8%; Pred. No. 1.7e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACCTGAGAGAGAGGCTGCTCTTACTACACCATTTTAACTTTCTTCTGAATTCAT 687
DB 453 AGCTGAGAGAGAGGCTGCTCTTACTACACCATTTTAACTTTCTTCTGAATTCAT 394
QY 688 TACTTCCTGTAGATTAAGTTCT 709
DB 393 TACTTCCTGTAGATTAAGTTCT 372

RESULT 26
US-10-450-763-2768/C
Sequence 2768, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 2768
LENGTH: 999
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (373)..(453)
OTHER INFORMATION: 100% homologous to Mus musculus UNK3, accession number
US-10-450-763-2768

Query Match 10.1%; Score 80.4; DB 10; Length 999;
Best Local Similarity 98.8%; Pred. No. 1.7e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACCTGAGAGAGAGGCTGCTCTTACTACACCATTTTAACTTTCTTCTGAATTCAT 687
DB 453 AGCTGAGAGAGAGGCTGCTCTTACTACACCATTTTAACTTTCTTCTGAATTCAT 394
QY 688 TACTTCCTGTAGATTAAGTTCT 709
DB 393 TACTTCCTGTAGATTAAGTTCT 372

RESULT 27
US-10-450-763-11488/C
Sequence 11488, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 11488
LENGTH: 1111
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (25)..(1452)
OTHER INFORMATION: 81% homologous to Homo sapiens putative p150, accession number
US-10-450-763-11488

Query Match 10.1%; Score 80.4; DB 10; Length 1111;

Best Local Similarity 98.8%; Pred. No. 1.8e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 628 ACCTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAAATTCAT 687
DB 453 AGCTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAAATTCAT 394

QY 688 TACTCTCTTGTAGTAAGTTCT 709
DB 393 TACTCTCTTGTAGTAAGTTCT 372

RESULT 28

US-09-909-650A-22/c
Sequence 22, Application US/09909650A
Patent No. US20020165386A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Inc.
APPLICANT: Fournier, Alain
APPLICANT: Maury, Isabelle
APPLICANT: Zhou-Liu, Qing
TITLE OF INVENTION: Desanlis-Cremont, Francine
FILE REFERENCE: ST99003-US-CNT-1
CURRENT APPLICATION NUMBER: US/09/909,650A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/FR00/00104
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/122,175
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 99/00586
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 1306
TYPE: DNA
ORGANISM: homo sapiens
US-09-909-650A-22

Query Match 10.1%; Score 80.4; DB 3; Length 1306;
Best Local Similarity 98.8%; Pred. No. 2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAAATTCATTA 689
DB 1279 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAAATTCATTA 1220
QY 690 CTTCCTTGTAGTAAGTTCTGT 711
DB 1219 CTTCCTTGTAGTAAGTTCTTT 1198

RESULT 29

US-09-165-522-4/c
Sequence 4, Application US/09165522
Publication No. US20030023950A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Paako
APPLICANT: Whitmarsh, Alan
APPLICANT: Yuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Faase, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1773 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 92...1357
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-165-522-4

Query Match 10.1%; Score 80.4; DB 3; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAAATTCATTA 689
DB 1343 CTGAGGAGAGAGGCTGCTCTTTACTACACCATTTTGTCTTTCTTCTGAAATTCATTA 1284
QY 690 CTTCCTTGTAGTAAGTTCTGT 711
DB 1283 CTTCCTTGTAGTAAGTTCTTT 1262

RESULT 30

US-10-343-710-54/c
Sequence 54, Application US/10343710
Publication No. US20040087478A1
GENERAL INFORMATION:
APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WENNDT, Stephan
APPLICANT: WEIHE, E.
APPLICANT: SCHAEFER, M., K.-H.
TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
CURRENT APPLICATION NUMBER: US/10/343,710
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
SEQ ID NO 54
LENGTH: 1773
TYPE: DNA
ORGANISM: Homo sapiens
US-10-343-710-54

Query Match 10.1%; Score 80.4; DB 8; Length 1773;
Best Local Similarity 98.8%; Pred. No. 2.2e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTCTTGAAATTCATTA 689
 DB 1343 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTCTTGAAATTCATTA 1284
 OY 690 CTTCCTGTAGATTAAGTTCTGT 711
 DB 1283 CTTCCTGTAGATTAAGTTCTTT 1262

RESULT 31

US-11-180-044-4/c
 ; Sequence 4, Application US/11180044
 ; Publication No. US20060035303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Roger J.
 ; APPLICANT: Flavell, Richard A.
 ; APPLICANT: Rakic, Pasko
 ; APPLICANT: Whitmarsh, Alan
 ; APPLICANT: Yang, Di
 ; APPLICANT: Yang, Di
 ; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/11/180,044
 ; FILING DATE: 12-JULY-2005
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/165,522
 ; FILING DATE: 02-Oct-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/060,995
 ; FILING DATE: 03-Oct-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Faese, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 10363/005001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1773 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 92...1357
 ; US-11-180-044-4

Query Match 10.1%; Score 80.4; DB 16; Length 1773;
 Best Local Similarity 98.8%; Pred. No. 2.2e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTCTTGAAATTCATTA 689
 DB 1343 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTCTTGAAATTCATTA 1284
 OY 690 CTTCCTGTAGATTAAGTTCTGT 711
 DB 1283 CTTCCTGTAGATTAAGTTCTTT 1262

DB 1283 CTTCCTGTAGATTAAGTTCTTT 1262

RESULT 32

US-10-450-763-19249/c
 ; Sequence 19249, Application US/10450763
 ; Publication No. US20050196754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HySeq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 790CIP3/US
 ; CURRENT APPLICATION NUMBER: US/10/450,763
 ; CURRENT FILING DATE: 2003-06-11
 ; PRIOR APPLICATION NUMBER: PCT/US01/08631
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: 09/540,217
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: 09/649,167
 ; PRIOR FILING DATE: 2000-08-23
 ; NUMBER OF SEQ ID NOS: 60736
 ; SOFTWARE: Custom
 ; SEQ ID NO 19249
 ; LENGTH: 1872
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIMILAR
 ; LOCATION: (1563)..(1688)
 ; OTHER INFORMATION: 80% homologous to Homo sapiens Human secreted protein, SEQ ID
 ; OTHER INFORMATION: NO: 7131, accession number G03050, Smith-Waterman Score=173.
 ; US-10-450-763-19249

Query Match 10.1%; Score 80.4; DB 10; Length 1872;
 Best Local Similarity 98.8%; Pred. No. 2.3e-08;
 Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 628 ACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTCTTGAAATTCAT 687
 DB 453 ACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTCTTGAAATTCAT 394
 OY 688 TACTTCCTGTAGATTAAGTTCT 709
 DB 393 TACTTCCTGTAGATTAAGTTCT 372

RESULT 33

US-09-771-161A-87/c
 ; Sequence 87, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 87
 ; LENGTH: 2131
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: (1)..(2131)
 ; LOCATION: (1)..(2131)
 ; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
 ; US-09-771-161A-87


```

; NAME: Faese, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 10363/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 224...1489
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-165-522-7

Query Match
Best Local Similarity 98.8%; Score 80.4; DB 3; Length 2372;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTCTGAATTCATTA 689
Db 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTCTGAATTCATTA 1416

Qy 690 CTTCCTTGATAGTAAGTTCTGT 711
Db 1415 CTTCCTTGATAGTAAGTTCTTT 1394

RESULT 37
US-10-305-720-1389/c
; Sequence 1389, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Sellhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO: 1389
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 9468150
US-10-305-720-1389

Query Match
Best Local Similarity 98.8%; Score 80.4; DB 7; Length 2372;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTCTGAATTCATTA 689
Db 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTCTGAATTCATTA 1416

Qy 690 CTTCCTTGATAGTAAGTTCTGT 711
Db 1415 CTTCCTTGATAGTAAGTTCTTT 1394

RESULT 38
US-10-466-162-5/c
; Sequence 5, Application US/10466162
; Publication No. US20050170343A1
```

```

; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling
; FILE REFERENCE: EX02-001C-PC
; CURRENT APPLICATION NUMBER: US/10/466,162
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 60/261,335
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,694
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,532
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,361
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,531
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,457
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,226
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,304
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,459
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,456
; PRIOR FILING DATE: 2001-01-12
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-466-162-5

Query Match
Best Local Similarity 98.8%; Score 80.4; DB 10; Length 2372;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTCTGAATTCATTA 689
Db 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTCTTTCTTCTGAATTCATTA 1416

Qy 690 CTTCCTTGATAGTAAGTTCTGT 711
Db 1415 CTTCCTTGATAGTAAGTTCTTT 1394

RESULT 39
US-10-723-681-9/c
; Sequence 9, Application US/10723681
; Publication No. US20050192239A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: KENELAND, RIKARD
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND
; FILE REFERENCE: SEO-4069-CP
; CURRENT APPLICATION NUMBER: US/10/723,681
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US 60/429,136
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 60/490,234
; PRIOR FILING DATE: 2003-07-24
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 9
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-10-723-681-9

Query Match 10.1%; Score 80.4; DB 10; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 1415 CTTCCTGTAGATAGTCTTT 1394

RESULT 40

US-10-857-780-11/c
Sequence 11, Application US/10857780
Publication No. US20050272043A1

GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RICHARD HENRY
APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens

US-10-857-780-11

Query Match 10.1%; Score 80.4; DB 10; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 1415 CTTCCTGTAGATAGTCTTT 1394

RESULT 41

US-11-127-817-9/c
Sequence 9, Application US/11127817
Publication No. US20050287519A1

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koentraad F. F.
APPLICANT: laenen, Wendy
TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-D USA
CURRENT APPLICATION NUMBER: US/11/127,817
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352

PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 534
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens

US-11-127-817-9

Query Match 10.1%; Score 80.4; DB 15; Length 2372;
Best Local Similarity 98.8%; Pred. No. 2.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1416
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 1415 CTTCCTGTAGATAGTCTTT 1394

RESULT 42

US-11-180-044-6/c
Sequence 6, Application US/11180044
Publication No. US20060035303A1

GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Pasko
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi
APPLICANT: Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/180,044
FILING DATE: 12-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-11-180-044-6

Query Match 10.1%; Score 80.4; DB 16; Length 2372;

Best Local Similarity 98.8%; Pred. No. 2.6e-08;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTTCTGAAATTCATTA 689

DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTTCTGAAATTCATTA 1416

QY 690 CTTCTGTAGATAAGTTCTGT 711

DB 1415 CTTCTGTAGATAAGTTCTTT 1394

RESULT 43

US-11-180-044-7/c

Sequence 7, Application US/11180044

Publication No. US2006035303A1

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.

APPLICANT: Flavell, Richard A.

APPLICANT: Rakic, Pasiko

APPLICANT: Whitmarsh, Alan

APPLICANT: Kuan, Chia-Yi

TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: IBM Compatible

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/180,044

FILING DATE: 12-JULY-2005

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/165,522

FILING DATE: 02-Oct-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/060,995

FILING DATE: 03-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 10363/005001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 224...1489

US-11-180-044-7

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTTCTGAAATTCATTA 689

DB 1475 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTTCTGAAATTCATTA 1416

QY 690 CTTCTGTAGATAAGTTCTGT 711

DB 1415 CTTCTGTAGATAAGTTCTTT 1394

RESULT 44

US-10-765-700-33/c

Sequence 33, Application US/10765700

Publication No. US20050130171A1

GENERAL INFORMATION:

APPLICANT: Loring, Jeanne F.

APPLICANT: Tingley, Debora W.

APPLICANT: Edwards, Carla M.

TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

FILE REFERENCE: PA-0024 US

CURRENT APPLICATION NUMBER: US/10/765,700

CURRENT FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: US/09/566,921

PRIOR FILING DATE: PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 138

SOFTWARE: PERL Program

SEQ ID NO 33

LENGTH: 2982

TYPE: DNA

ORGANISM: Homo sapiens

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No: 413797.7

FEATURE:

NAME/KEY: unsure

LOCATION: 1770-1816

OTHER INFORMATION: a, t, c, g, or other

US-10-765-700-33

Query Match 10.1%; Score 80.4; DB 10; Length 2982;

Best Local Similarity 98.8%; Pred. No. 2.8e-08;

Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTTCTGAAATTCATTA 689

DB 1570 CTGAAGAGAGAGGCTGCTCTTTACTACACATTTTACTCTTCTTCTGAAATTCATTA 1511

QY 690 CTTCTGTAGATAAGTTCTGT 711

DB 1510 CTTCTGTAGATAAGTTCTTT 1489

RESULT 45

US-09-776-167A-8/c

Sequence 8, Application US/09776167A

Patent No. US20020058243A1

GENERAL INFORMATION:

APPLICANT: Jarnigan, Kurt

APPLICANT: Greene, Amy

TITLE OF INVENTION: RAPID, PARALLEL IDENTIFICATION OF CELL LINES

FILE REFERENCE: 0024 US

CURRENT APPLICATION NUMBER: US/09/776,167A

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: USSN 60/179,893

PRIOR FILING DATE: 2000-02-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 8750

TYPE: DNA

ORGANISM: pFastFind-JNK3

US-09-776-167A-8

Query Match 10.1%; Score 80.4; DB 3; Length 8750;

Best Local Similarity 98.8%; Pred. No. 4.6e-08;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 630 CTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 689
Db 1782 CTGAAGAGAGAGGCTGCTCTTCTTACTACACCATTTTACTCTTCTTCTGAAATTCATTA 1723

Qy 690 CTTCCTTGTAGATAGTTCTGT 711
Db 1722 CTTCCTTGTAGATAGTTCTTT 1701

RESULT 46

US-11-136-527-4334/c
Sequence 4334, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4334
LENGTH: 600
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-4334

Query Match 8.3%; Score 66.8; DB 16; Length 600;
Best Local Similarity 86.0%; Pred. No. 2.4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 636 GTACCTGAAGAGAGGCTGCTCTTCTTACTACACCATTTTACTCTTCTTCTGAAATTC 685
Db 125 GCACCTGAAGAGGCTGCTGCTTGTACTACCGCGTCTTCTTCTTCTGAGTTTC 66

Qy 686 ATTACTCTCTGTAGATAGTTCTGT 711
Db 65 ATTACTCTCTGTAGATAGTTCTTT 40

RESULT 47

US-09-165-522-9/c
Sequence 9, Application US/09165522
Publication No. US20030023990A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Flavell, Richard A.
APPLICANT: Rakic, Paeko
APPLICANT: Whitmarsh, Alan
APPLICANT: Kuan, Chia-Yi

TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522

FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,995
FILING DATE: 03-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Passe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10363/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 364...1641
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-165-522-9

Query Match 8.3%; Score 66.8; DB 3; Length 1975;
Best Local Similarity 86.0%; Pred. No. 4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGAGGCTGCTCTTCTTACTACACCATTTTACTCTTCTTCTGAAATTC 685
Db 1505 GCACCTGAAGAGGCTGCTGCTTGTACTACCGCGTCTTCTTCTTCTGAGTTTC 1446

Qy 686 ATTACTCTCTGTAGATAGTTCTGT 711
Db 1445 ATTACTCTCTGTAGATAGTTCTTT 1420

RESULT 48

US-10-343-710-60/c
Sequence 60, Application US/10343710
Publication No. US20040087478A1
GENERAL INFORMATION:
APPLICANT: GILLEN, Clemens
APPLICANT: WETZELS, Ingrid
APPLICANT: WENDEL, Stephan
APPLICANT: WEIHE, E.
APPLICANT: SCHAEFER, M., K.-H.
TITLE OF INVENTION: SCREENING METHOD
FILE REFERENCE: 029310.52022US
CURRENT APPLICATION NUMBER: US/10/343, 710
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP01/09011
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn version 3.2
SEQ ID NO 60
LENGTH: 1975
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-343-710-60

Query Match 8.3%; Score 66.8; DB 8; Length 1975;
Best Local Similarity 86.0%; Pred. No. 4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 626 GTACCTGAAGAGAGGCTGCTCTTCTTACTACACCATTTTACTCTTCTTCTGAAATTC 685
Db 1505 GCACCTGAAGAGGCTGCTGCTTGTACTACCGCGTCTTCTTCTTCTGAGTTTC 1446

Qy 686 ATTACTCTCTGTAGATAGTTCTGT 711
Db 1445 ATTACTCTCTGTAGATAGTTCTTT 1420

RESULT 49

```
US-11-180-044-9/c
; Sequence 9, Application US/11180044
; Publication No. US20060035303A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Flavell, Richard A.
; APPLICANT: Rakic, Pasko
; APPLICANT: Whitmarsh, Alan
; APPLICANT: Kuan, Chia-Yi
; APPLICANT: Yang, Di
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/180,044
; FILING DATE: 12-JULY-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,522
; FILING DATE: 02-Oct-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,995
; FILING DATE: 03-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 10363/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 364...1641
; US-11-180-044-9

Query Match      8.3%; Score 66.8; DB 16; Length 1975;
Best Local Similarity 86.0%; Pred. No. 4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy      626 GTACCTGAAGAGAGAGCTGTCCTTTTACTACACCAATTTTGTCTTCTTGAAATC 685
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1505 GCACCTGAAGGTGAGGGGTGGCTTTGACTACGCCGTTCTTCTTCTTGAGTTC 1446

Qy      686 ATTACTCTCTGTAGATAGTTCCTGT 711
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1445 ATTACTCTCTGTAGATGAGTTCCTT 1420

RESULT 50
US-11-136-527-238/c
; Sequence 238, Application US/11136527
; Publication No. US20050287570A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 238
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-238

Query Match      8.3%; Score 66.8; DB 16; Length 1980;
Best Local Similarity 86.0%; Pred. No. 4e-05;
Matches 74; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy      626 GTACCTGAAGAGAGAGCTGTCCTTTTACTACACCAATTTTGTCTTCTTGAAATC 685
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1505 GCACCTGAAGGTGAGGGGTGGCTTTGACTACGCCGTTCTTCTTCTTGAGTTC 1446

Qy      686 ATTACTCTCTGTAGATAGTTCCTGT 711
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1445 ATTACTCTCTGTAGATGAGTTCCTT 1420
```

Search completed: July 19, 2006, 23:05:29
Job time : 1478 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 19:46:54 ; Search time 166 Seconds
(without alignments)
6923.085 Million cell updates/sec

Title: US10723681MOD.SEQ

Perfect score: 800
Sequence: 1 accctttcccaaacctctta.....caataatcagcttttgatg 800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 899801 seqs, 718270062 residues

Total number of hits satisfying chosen parameters: 1799602

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA New.*
1: /EMC_Celerra_SIDS3/prodata/1/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/prodata/1/pubpna/US10_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq.*
9: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	82.8	10.3	1000	US-11-266-748A-223967	Sequence 223967, A
C 2	82.8	10.3	1000	US-11-266-748A-292324	Sequence 292324, A
C 3	82.8	10.3	1000	US-11-266-748A-343753	Sequence 343753, A
C 4	82.8	10.3	1000	US-11-266-748A-403979	Sequence 403979, A
C 5	82.8	10.3	1000	US-11-266-748A-403980	Sequence 403980, A
C 6	82.8	10.3	1000	US-11-266-748A-475025	Sequence 475025, A
C 7	82.8	10.3	1000	US-11-266-748A-475026	Sequence 475026, A
C 8	82.8	10.3	2211	US-11-266-748A-571178	Sequence 571178, A
C 9	82.8	10.3	2698	US-11-266-748A-31164	Sequence 31164, A
C 10	82.8	10.3	3232	US-11-266-748A-349578	Sequence 349578, A
C 11	82.8	10.3	3232	US-11-266-748A-382414	Sequence 382414, A
C 12	82.8	10.3	3232	US-11-266-748A-432957	Sequence 432957, A
C 13	50	6.2	801	US-11-266-748A-469808	Sequence 469808, A
C 14	48.4	6.0	1000	US-11-266-748A-403999	Sequence 403999, A
C 15	48.4	6.0	1000	US-11-266-748A-475045	Sequence 475045, A
C 16	48.4	6.0	1180	US-11-266-748A-69204	Sequence 69204, A
C 17	48.4	6.0	1180	US-11-266-748A-105295	Sequence 105295, A
C 18	48.4	6.0	1180	US-11-266-748A-132015	Sequence 132015, A
C 19	48.4	6.0	1928	US-11-266-748A-349867	Sequence 349867, A
C 20	48.4	6.0	1928	US-11-266-748A-452866	Sequence 452866, A
C 21	48.4	6.0	1942	US-11-283-329-221	Sequence 221, App
C 22	48.4	6.0	1942	US-11-283-329-225	Sequence 225, App
C 23	48.4	6.0	2251	US-11-266-748A-182241	Sequence 182241, A
C 24	48.4	6.0	2251	US-11-266-748A-242782	Sequence 242782, A
C 25	46.8	5.8	1947	US-11-283-329-227	Sequence 227, App
C 26	46.8	5.8	1947	US-11-283-329-229	Sequence 229, App
C 27	44.4	5.5	1412	US-11-283-329-217	Sequence 217, App
C 28	44.4	5.5	1412	US-11-283-329-223	Sequence 223, App
C 29	43.2	5.4	1676	US-10-449-902-24462	Sequence 24462, A
C 30	42	5.2	1000	US-11-266-748A-395934	Sequence 395934, A
C 31	42	5.2	1000	US-11-266-748A-466980	Sequence 466980, A
C 32	42	5.2	1417	US-11-283-329-219	Sequence 219, App
C 33	42	5.2	1417	US-11-283-329-221	Sequence 221, App
C 34	42	5.2	1943	US-11-266-748A-349577	Sequence 349577, A
C 35	42	5.2	1943	US-11-266-748A-382413	Sequence 382413, A
C 36	42	5.2	1943	US-11-266-748A-432956	Sequence 432956, A
C 37	42	5.2	3620	US-11-266-748A-243382	Sequence 243382, A
C 38	41.2	5.2	807	US-11-216-545-1069	Sequence 1069, A
C 39	41	5.1	570	US-11-266-748A-207992	Sequence 207992, A
C 40	40.8	5.1	139326	US-10-539-228-134	Sequence 134, App
C 41	40.4	5.0	1582	US-11-222-810-10	Sequence 10, App1
C 42	40.4	5.0	1582	US-11-222-810-12	Sequence 12, App1
C 43	39.6	5.0	557	US-11-266-748A-41216	Sequence 41216, A
C 44	39.6	5.0	559	US-11-266-748A-95203	Sequence 95203, A
C 45	39.6	5.0	559	US-11-266-748A-148014	Sequence 148014, A
C 46	39.6	5.0	1000	US-11-266-748A-117427	Sequence 117427, A
C 47	39.6	5.0	1000	US-11-266-748A-159591	Sequence 159591, A
C 48	39.6	5.0	1000	US-11-266-748A-222651	Sequence 222651, A
C 49	39.6	5.0	1000	US-11-266-748A-289193	Sequence 289193, A
C 50	39.6	5.0	1000	US-11-266-748A-340622	Sequence 340622, A
C 51	39.6	5.0	1000	US-11-266-748A-400178	Sequence 400178, A
C 52	39.6	5.0	1000	US-11-266-748A-471224	Sequence 471224, A
C 53	39.6	5.0	3091	US-10-517-441-483	Sequence 483, App
C 54	39.6	5.0	3091	US-10-517-441-757	Sequence 757, App
C 55	39.6	5.0	3216	US-10-511-937-609	Sequence 609, App
C 56	39.6	5.0	6101	US-10-517-441-705	Sequence 705, App
C 57	39.2	4.9	11429	US-10-517-441-460	Sequence 460, App
C 58	39.2	4.9	11429	US-10-517-441-754	Sequence 754, App
C 59	38.6	4.8	1973	US-11-216-545-582	Sequence 582, App
C 60	38.6	4.8	8900	US-10-517-441-427	Sequence 427, App
C 61	38.6	4.8	8900	US-10-517-441-701	Sequence 701, App
C 62	38.4	4.8	604	US-11-266-748A-51538	Sequence 51538, A
C 63	38.4	4.8	661	US-11-266-748A-12709	Sequence 12709, A
C 64	38.4	4.8	1000	US-11-266-748A-291112	Sequence 291112, A
C 65	38.4	4.8	1000	US-11-266-748A-34251	Sequence 34251, A
C 66	38.4	4.8	1000	US-11-266-748A-402493	Sequence 402493, A
C 67	38.4	4.8	1000	US-11-266-748A-473539	Sequence 473539, A
C 68	38.4	4.8	1228	US-11-266-748A-189872	Sequence 189872, A
C 69	38.4	4.8	1228	US-11-266-748A-243474	Sequence 243474, A
C 70	38.4	4.8	2875	US-11-266-748A-30798	Sequence 30798, A
C 71	38	4.8	852	US-11-216-545-385	Sequence 385, App
C 72	38	4.8	6101	US-10-517-441-431	Sequence 431, App
C 73	37.8	4.7	4181	US-10-486-020-36	Sequence 36, App1
C 74	37.8	4.7	8093	US-10-517-441-308	Sequence 308, App
C 75	37.8	4.7	8093	US-10-517-441-562	Sequence 562, App
C 76	37.8	4.7	162354	US-11-266-748A-334317	Sequence 234317, A
C 77	37.6	4.7	394191	US-10-506-549-3	Sequence 3, App1
C 78	37.6	4.7	945	US-10-471-571A-1599	Sequence 1599, App
C 79	37.4	4.7	1349	US-11-266-748A-25400	Sequence 180936, A
C 80	37.4	4.7	19334	US-11-266-748A-25400	Sequence 25400, A
C 81	37.4	4.7	19334	US-10-517-441-414	Sequence 414, App
C 82	37.4	4.7	19334	US-10-517-441-688	Sequence 688, App
C 83	37.2	4.7	8169	US-10-517-441-270	Sequence 270, App
C 84	37.2	4.7	8169	US-10-517-441-544	Sequence 544, App
C 85	36.8	4.6	1000	US-11-266-748A-116732	Sequence 116732, A
C 86	36.8	4.6	1000	US-11-266-748A-158896	Sequence 158896, A
C 87	36.8	4.6	1000	US-11-266-748A-158896	Sequence 158896, A
C 88	36.8	4.6	1000	US-11-266-748A-181979	Sequence 181979, A
C 89	36.8	4.6	1000	US-11-266-748A-308619	Sequence 308619, A
C 90	36.8	4.6	1649	US-11-216-545-514	Sequence 514, App
C 91	36.8	4.6	2630	US-11-266-748A-177342	Sequence 27342, App
C 92	36.6	4.6	879	US-10-471-571A-1881	Sequence 1881, App
C 93	36.6	4.6	1607	US-11-216-545-1584	Sequence 1584, App
C 94	36.6	4.6	2444	US-11-216-305-15168	Sequence 15168, A
C 95	36.6	4.6	150024	US-11-266-748A-60111	Sequence 60111, A
C 96	36.4	4.5	4294	US-11-021-837-14	Sequence 14, App1
C 97	36.4	4.5	4443	US-11-266-748A-24099	Sequence 24099, A

C 98 36.4 4.5 13076 6 US-10-517-441-394 Sequence 394, App
C 99 36.4 4.5 13076 6 US-10-517-441-668 Sequence 668, App
C 100 36.2 4.5 2707 8 US-11-216-545-2975 Sequence 2975, Ap

ALIGNMENTS

RESULT 1

US-11-266-748A-223967/c
; Sequence 223967, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Hatkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 223967
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-223967
Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GACCTGAAGAGGAGGCTGCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTC 685
DB 112 GCACCTGAAGAGGAGGCTGCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTC 53
QY 686 ATTACTTCCTTGATAGTATGTTCTGT 711
DB 52 ATTACTTCCTTGATAGTATGTTCTTT 27
RESULT 2
US-11-266-748A-292324/c
; Sequence 292324, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Hatkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 292324
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-292324

Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 626 GACCTGAAGAGGAGGCTGCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTC 685
DB 112 GCACCTGAAGAGGAGGCTGCTTTTACTACACCAATTTTGTCTTTCTTCTGAATTC 53
QY 686 ATTACTTCCTTGATAGTATGTTCTGT 711
DB 52 ATTACTTCCTTGATAGTATGTTCTTT 27

RESULT 3

US-11-266-748A-343753
; Sequence 343753, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Hatkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 343753
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-343753
Query Match 10.3%; Score 82.8; DB 8; Length 1000;

```
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
    |||||
DB 889 GCACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 948

QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
    |||||
DB 949 ATTACTCTCTGTAGATAGTTCTTT 974

RESULT 4
US-11-266-748A-403979/c
; Sequence 403979, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 403979
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-403979

Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
    |||||
DB 112 GCACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 53

QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
    |||||
DB 52 ATTACTCTCTGTAGATAGTTCTTT 27

RESULT 5
US-11-266-748A-403980/c
; Sequence 403980, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 403980
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-403980

Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 403980
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-403980

Query Match 10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
    |||||
DB 112 GCACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTACTCTTTCTTCTGAATTC 53

QY 686 ATTACTCTCTGTAGATAGTTCTGT 711
    |||||
DB 52 ATTACTCTCTGTAGATAGTTCTTT 27

RESULT 6
US-11-266-748A-475025
; Sequence 475025, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 475025
; LENGTH: 1000
; TYPE: DNA
```

```

; ORGANISM: Homo Sapiens
US-11-266-748A-475026

Query Match          10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTTCTTGAATTC 685
    |||
DB 889 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTTCTTGAATTC 948
    |||

QY 686 ATTACTCTCTGTAGATAGTCTGT 711
    |||
DB 949 ATTACTCTCTGTAGATAGTCTTT 974
    |||

RESULT 7
US-11-266-748A-475026
; Sequence 475026, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 475026
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-475026

Query Match          10.3%; Score 82.8; DB 8; Length 1000;
Best Local Similarity 97.7%; Pred. No. 1.3e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTTCTTGAATTC 685
    |||
DB 889 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTTCTTGAATTC 948
    |||

QY 686 ATTACTCTCTGTAGATAGTCTGT 711
    |||
DB 949 ATTACTCTCTGTAGATAGTCTTT 974
    |||

RESULT 8
US-11-266-748A-57178/C
; Sequence 57178, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
```

```

; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: US/11/266,748A
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57178
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-57178

Query Match          10.3%; Score 82.8; DB 8; Length 2211;
Best Local Similarity 97.7%; Pred. No. 1.6e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTTCTTGAATTC 685
    |||
DB 1323 GCACCTGAAGAGGAGGCTGCTCTTTTACTACACCATTTTGTCTTTTCTTGAATTC 1264
    |||

QY 686 ATTACTCTCTGTAGATAGTCTGT 711
    |||
DB 1263 ATTACTCTCTGTAGATAGTCTTT 1238
    |||

RESULT 9
US-11-266-748A-31164/C
; Sequence 31164, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: US/11/266,748A
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
```

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31164
; LENGTH: 2698
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-31164

Query Match      10.3%; Score 82.8; DB 8; Length 2698;
Best Local Similarity 97.7%; Pred. No. 1.7e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626  GACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
      |||||||
DB      1810  GCACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 1751

QY      686  ATTACTCTCTGTAGATTAAGTTCTGT 711
      |||||||
DB      1750  ATTACTCTCTGTAGATTAAGTTCTTT 1725

RESULT 10
US-11-266-748A-349578/c
; Sequence 349578, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptional Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 349578
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (161)..(201)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1975)..(2028)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-349578

Query Match      10.3%; Score 82.8; DB 8; Length 3232;
Best Local Similarity 97.7%; Pred. No. 1.8e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626  GACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
      |||||||
DB      1788  GCACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 1729
```

```

QY      686  ATTACTCTCTGTAGATTAAGTTCTGT 711
      |||||||
DB      1728  ATTACTCTCTGTAGATTAAGTTCTTT 1703

RESULT 11
US-11-266-748A-382414/c
; Sequence 382414, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptional Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 382414
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (161)..(201)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1975)..(2028)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-382414

Query Match      10.3%; Score 82.8; DB 8; Length 3232;
Best Local Similarity 97.7%; Pred. No. 1.8e-10;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      626  GACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 685
      |||||||
DB      1788  GCACCTGAAGAGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTC 1729

QY      686  ATTACTCTCTGTAGATTAAGTTCTGT 711
      |||||||
DB      1728  ATTACTCTCTGTAGATTAAGTTCTTT 1703

RESULT 12
US-11-266-748A-432957
; Sequence 432957, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptional Microarray Technology and
```

```
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 432957
LENGTH: 3232
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1205)..(1254)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc.feature
LOCATION: (3032)..(3072)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-432957

Query Match
Best Local Similarity 10.3%; Score 82.8; DB 8; Length 3232;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 626 GTACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTGTCTTTCTTGAATTC 685
Db 1445 GCACCTGAAGAGGAGGCTGCTTTTACTACACCATTTTGTCTTTCTTGAATTC 1504
Qy 686 ATTACTCTGTAGATTAAGTCTGT 711
Db 1505 ATTACTCTGTAGATTAAGTCTGT 1530

RESULT 13
US-11-266-748A-46908/c
Sequence 46908, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcription Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 403999
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-403999
```

```
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 46908
LENGTH: 801
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-46908
```

```
Query Match
Best Local Similarity 6.2%; Score 50; DB 8; Length 801;
Matches 62; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
```

```
Qy 630 CTGAAGAGAGGAGGCTGCTTTTACTACACCATTTTGTCTTTCTTGAATTCATTA 689
Db 431 CTGCATCTGAAGAGGCTGATCTTTTACTACACCATTTCTTCTTCCCAATCATGA 372
Qy 690 CTTCCTGTAGATTAAGTCTGT 711
Db 371 CTTCCTGTAGATTAAGTCTGT 350
```

```
RESULT 14
US-11-266-748A-403999/c
Sequence 403999, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcription Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 403999
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-403999

Query Match
Best Local Similarity 6.0%; Score 48.4; DB 8; Length 1000;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```

```
RESULT 15
US-11-266-748A-475045
; Sequence 475045, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 475045
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-475045

Query Match      6.0%; Score 48.4; DB 8; Length 1000;
Best Local Similarity 74.4%; Pred. No. 0.028;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAAATTCATTA 689
DB      756 CTGCATCTGAAGGCTGATCTTTTACACACCAATTTCTGCTTTCTTCCCAATCCATCA 815

QY      690 CTTCCTGTAGATAAGTCTGT 711
DB      816 CTTCTTTGTAATTAATGCTCTTT 837

RESULT 16
US-11-266-748A-69204/C
; Sequence 69204, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
```

```
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69204
; LENGTH: 1180
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-69204

Query Match      6.0%; Score 48.4; DB 8; Length 1180;
Best Local Similarity 74.4%; Pred. No. 0.03;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAAATTCATTA 689
DB      431 CTGCATCTGAAGGCTGATCTTTTACACACCAATTTCTGCTTTCTTCCCAATCCATCA 372

QY      690 CTTCCTGTAGATAAGTCTGT 711
DB      371 CTTCTTTGTAATTAATGCTCTTT 350

RESULT 17
US-11-266-748A-105295/C
; Sequence 105295, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105295
; LENGTH: 1180
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-105295

Query Match      6.0%; Score 48.4; DB 8; Length 1180;
Best Local Similarity 74.4%; Pred. No. 0.03;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      630 CTGAAGAGAGAGGCTGCTCTTTACTACACCAATTTTACTGCTTTCTTCTGAAATTCATTA 689
DB      431 CTGCATCTGAAGGCTGATCTTTTACACACCAATTTCTGCTTTCTTCCCAATCCATCA 372
```


Qy ,	690	CTTCCTTGTAGATAAGTTCTGT	711
Db	371	CTTCCTTGTAAATTAGCTCTTT	350

RESULT 18
US-11-266-748A-122015

```

Sequence 122015, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Hartlin, Paul
APPLICANT: Johnson, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptional Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIORITY APPLICATION NUMBER: EP 04105479.2
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105482.6
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105483.4
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105507.0
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105485.9
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105484.2
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: US 60/662,276
PRIORITY FILING DATE: 2005-03-14
PRIORITY APPLICATION NUMBER: US 60/700,293
PRIORITY FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 122015
LENGTH: 1180
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-122015

```

Query Match	6.0%;	Score 48.4;	DB 8;	Length 1180;
Best Local Similarity	74.4%;	Pred. No. 0.03;		
Matches	61;	Conservative	0;	Mismatches 21;
				Indels 0;
				Gaps 0

QY	690	CTTCCTGTAGATAAGTTCTGT	711
Db	810	CTTCTTTGTAATTAGCTCTTT	831

RESULT 19
US-11-266-748A-349487/C
Sequence 349487, Application US/11266748A
Publication No. US20060134653A1
GENERAL INFORMATION:
APPLICANT: Hartin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transciptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (31/9189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
PRIORITY FILING DATE: 2005-11-03
PRIORITY APPLICATION NUMBER: EP 04105479.2
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105482.6
PRIORITY FILING DATE: 2004-11-03

```

1 PRIOR APPLICATION NUMBER: EP 04105483.4
2 PRIOR FILING DATE: 2004-11-03
3 PRIOR APPLICATION NUMBER: EP 04105507.0
4 PRIOR FILING DATE: 2004-11-03
5 PRIOR APPLICATION NUMBER: EP 04105485.5
6 PRIOR FILING DATE: 2004-11-03
7 PRIOR APPLICATION NUMBER: EP 04105484.2
8 PRIOR FILING DATE: 2004-11-03
9 PRIOR APPLICATION NUMBER: US 60/662,276
10 PRIOR FILING DATE: 2005-03-14
11 PRIOR APPLICATION NUMBER: US 60/700,293
12 PRIOR FILING DATE: 2005-07-18
13 NUMBER OF SEQ ID NOS: 483996
14 SOFTWARE: PatentIn version 3.3
15 SEQ ID NO 349487
16 LENGTH: 1928
17 TYPE: DNA
18 ORGANISM: Homo Sapiens
19 US-11-266-748A-349487

```

Query Match	6.0%	Score 48.4;	DB 8;	Length 1928;
Best Local Similarity	74.4%;	Pred. No. 0.035;		
Matches 61;	Conservative 0;	Mismatches 21;	Indels 0;	Gaps 0

QY		690	C TTCCTGTAGATAAGTTCGT	711
Dd		1126	CTTCCTTGTAATTAGCCTTT	1105

RESULT 20 748A-432866
US-11-266-748A-432866
Sequence 432866, Application US/11266748A
Publication NO. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Milligan, Karl
TITLE OF INVENTION: Transciptome Microarray Technology and
TITLE OF INVENTION: Method of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479, 2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482, 6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483, 4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507, 0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485, 9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484, 2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662, 276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700, 293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 432866
LENGTH: 1928
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-432866

Query Match	6.0%	Score 48.4;	DB 8;	Length 1928;
Best Local Similarity	74.4%	Pred. NO. 0.035;		
Matches	61;	Conservative	0;	Mismatches 21;
			Indels	0;
			Gaps	0

Qy	Dy	Qy	Dy
630	CTAAGAGAAAGGCTGCCCTTTACTACACGATTTTATGCTTTCTCTGAATCATTA	690	CTTCCTGTGATTAATGCTGT
743	CTGCATCTGAAGGCTATCTTTTACACACCATTCCTGCTTTCTTCCCAATCATGA	803	CTCTTTGTGAATTAAGCTCTTT

```

RESULT 21
US-11-283-329-225/c
: Sequence 225: Application US/11283329
: Publication No. US20060134670A1
: GENERAL INFORMATION:
: APPLICANT: Piu, Fabrizio
: TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
: TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
: FILE REFERENCE: ACADIA_043A
: CURRENT APPLICATION NUMBER: US/11/283,329
: CURRENT FILING DATE: 2005-11-18
: PRIOR APPLICATION NUMBER: 60/6129,811
: PRIOR FILING DATE: 2004-11-19
: NUMBER OF SEQ ID NOS: 242
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 225
: LENGTH: 1942
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (50)...(1324)
: OTHER INFORMATION: JUNK2 variant 1
: US-11-283-329-225

```

Query Match	6.0%	Score 48.4	DB 8	Length 1942
Best Local Similarity	74.4%	Pred. No. 0.035	Mismatches 21	Indels 0
Matches	61	Conservative	0	Gaps 0
Qy	630	CTGAAGAGAAAGGCGTCCTTTACTAACCATTTTAGCTCTTCTCTGAATCATTA	689	
Db	1187	CTGATCTGAAGGCGATCTTTTACAAACACATCTCTCTTCTCCCAATCARGA	1128	
Qy	690	CTTCCTGTAGATAAGTTCTGT	711	
Db	1127	CTTCTTTGTAAATTAAGCTCTTT	1106	

```

RESULT 22
US-11-283-329-231/c
Sequence 231, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrizio
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
FILE OF INVENTION: HORMONE NUCLEAR RECEPTORS
FILE REFERENCE: ACADIA_043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 231
LENGTH: 1942
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1334)
OTHER INFORMATION: JNK2 variant 4
US-11-283-329-231

```

Query	March		6.0%;	Score	48.4;	DB	8;	Length	1942;
Best Local Similarity		74.4%;	Pred.	No.	0.035;				
Matches	61;	Conservative	0;	Mismatches	21;	Indels	0;	Gaps	0;
Oy	630	CTGAAGAGAAGGCGTCCCTTTACTACACCATTATTTAGCTTTCTTCGTGAATTCATA	689						
Dd	1187	CTGCATCTGAAGGTATCTTTTACAAACACACATTCTTGCTTTCTTCCCACATCATGA	1128						
Oy	690	CTTCCCTGTGATAAAGTTCTGT	711						
Dd	1127	CTTCTTTGTAATTAAGCTCTTT	1106						

```

RESULT 23 US-11-266-748A-182241/c
US-11-266-748A-182241 Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Hartin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 182241
LENGTH: 2251
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-182241

```

	Query Match	6.0%;	Score 48.4;	DB 8;	Length 2251;
	Best Local Similarity	74.4%;	Pred. No.0.036;	Mismatches 21;	Indels 0; Gaps 0;
	Matches	61;	Conservative	0;	
Qy	630 CTGAAGAGAAGGCTGCCCTTTACTACAAACCATTATTTAGTCTTTCTTGCAATTCATTA	689			
Db	298 CTGCATCTGAAGGTGATCTTTTACAACACACATTCCTCTTCTTCCCAATCCATGA	239			
Qy	690 CTTCCCTGTGATAAATTCGT	711			
Db	238 CTCCTTGTGAAATTAATGCTCTTT	217			

RESULT 24
US-11-266-748A-242782
Sequence 242782, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transciphertext Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 242782
LENGTH: 2251
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-242782

Query Match 6.0%; Score 48.4; DB 8; Length 2251;
Best Local Similarity 74.4%; Pred. No. 0.036;
Matches 61; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 630 CTGACAGAGAGAGCTGCTCTTACTACACCATTTTGTCTTCTGCAATTCATTA 689
DB 1954 CTGCACTCTGAGAGCTATCTTTACACACCATTTCTTCTTCCCAATTCATGA 2013
QY 690 CTTCCTGTAGATAGTCTGT 711
DB 2014 CTTCCTGTAAATTAAGCTCTTT 2035

RESULT 25
US-11-283-329-227/c
Sequence 227, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 227
LENGTH: 1947
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1198)
OTHER INFORMATION: JNK2 variant 2
US-11-283-329-227

Query Match 5.8%; Score 46.8; DB 8; Length 1947;
Best Local Similarity 77.0%; Pred. No. 0.085;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 638 GAAGGCTGTCTTTACTACACCATTTTGTCTTCTGCAATTCATTCCTTG 697
DB 1179 GAAGGCTGTCTTTACTACACCATTTCTTCTTCCCAATTCATTCATCTTTG 1120

QY 698 TAGATPAAGTCTGT 711
DB 1119 TAAATTAAGCTCTTT 1106

RESULT 26
US-11-283-329-229/c
Sequence 229, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 229
LENGTH: 1947
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1198)
OTHER INFORMATION: JNK2 variant 3
US-11-283-329-229

Query Match 5.8%; Score 46.8; DB 8; Length 1947;
Best Local Similarity 77.0%; Pred. No. 0.085;
Matches 57; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 638 GAAGGCTGTCTTTACTACACCATTTTGTCTTCTGCAATTCATTCCTTG 697
DB 1179 GAAGGCTGTCTTTACTACACCATTTCTTCTTCCCAATTCATTCATCTTTG 1120
QY 698 TAGATPAAGTCTGT 711
DB 1119 TAAATTAAGCTCTTT 1106

RESULT 27
US-11-283-329-217/c
Sequence 217, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
FILE REFERENCE: ACADIA.043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 217
LENGTH: 1412
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (18)...(1301)
OTHER INFORMATION: JNK1 variant 1
US-11-283-329-217

Query Match 5.5%; Score 44.4; DB 8; Length 1412;
Best Local Similarity 69.8%; Pred. No. 0.29;
Matches 60; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 626 GTACTGAAGAGAGGCTGTCTTTACTACACCATTTTGTCTTCTTCTGCAATTC 685

Db 1159 GCACCTAAAGAGAGGGGCTCCCCCGTATACCTCCATCTTGTCTCTCTCCAGTCC 1100
QY 686 ATTACTTCTTGTAGTAACTTCTGT 711
Db 1099 ATAACTTCTTATATATCAATCTTT 1074

RESULT 28

US-11-283-329-223/C
; Sequence 223, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Plu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; PRIOR FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1301)
; OTHER INFORMATION: JUNK variant 4
US-11-283-329-223

Query Match 5.5%; Score 44.4; DB 8; Length 1412;
Best Local Similarity 69.8%; Pred. No. 0.29;
Matches 60; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 626 GTACCTGAAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAAATC 685
DB 1159 GCACCTAAAGAGAGGGCTCCCCCGTATACCTCCATCTTGTCTCTCTCCAGTCC 1100
QY 686 ATTACTTCTTGTAGTAACTTCTGT 711
DB 1099 ATAACTTCTTATATATCAATCTTT 1074

RESULT 29

US-10-449-902-24462/C
; Sequence 24462, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24462
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK099904
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24462

Query Match 5.4%; Score 43.2; DB 6; Length 1676;
Best Local Similarity 52.8%; Pred. No. 0.6;
Matches 93; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 408 ATGAATAAAGTTTGTGCTGATCATTTACCATCAGAAATATGAAATGACACACTG 467
DB 285 AAGAGAGTTTGTGCTGATCATTTACCATCAGAAATATGAAATGACACACTG 226
QY 468 AATATCAAAAGAAATATAAATCAATATTAAGACACAAACCATGTGATATTTGTCCA 527
DB 225 ATAAAT 166
QY 528 TGTGCTTTAAGCAATGTATGTTTCTTGCAACCCCTACACAAAGCCACAGA 583
DB 165 GCAGATTAATACCGCAATGTGAAGTATGTAAGAGGCACTAAATTAGAGAGGA 110

RESULT 30

US-11-266-748A-395934/C
; Sequence 395934, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 395934
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-395934

Query Match 5.2%; Score 42; DB 8; Length 1000;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 630 CTGAAGAGAGAGGCTGCTCTTACTACACCATTTTGTCTTCTCTGAAATCATA 689
DB 738 CTAAGAGAGAGGCTGCCCGCTATACCTCAATCTTGTCTCTCTCCAGTCCATXA 679
QY 690 CTTCTTGTAGATAAGTTCTGT 711
DB 678 CTTCTTATATATCAATCTTT 657

RESULT 31

US-11-266-748A-466980
; Sequence 466980, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

```

; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptional Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: Patent version 3.3
; SEQ ID NO 466980
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-466980

Query Match          5.2%; Score 42; DB 8; Length 1000;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```

```

QY 630 CTGAAGGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
    |||||
DB 263 CTTAAAGGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 322
    |||||
QY 690 CTTCTTGTAGATTAAGTTCTGT 711
    |||||
DB 323 CTTCTTGTATATATCAATTTCTTT 344
    |||||

```

```

RESULT 32
US-11-283-329-219/C
; Sequence 219, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1172)
; OTHER INFORMATION: UNK1 variant 2
US-11-283-329-219

```

```

Query Match          5.2%; Score 42; DB 8; Length 1417;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```

```

QY 630 CTGAAGGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
    |||||
DB 1155 CTTAAAGGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1096
    |||||
QY 690 CTTCTTGTAGATTAAGTTCTGT 711
    |||||
DB 1095 CTTCTTGTATATATCAATTTCTTT 1074
    |||||

```

```

RESULT 33
US-11-283-329-221/C
; Sequence 221, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(1172)
; OTHER INFORMATION: UNK1 variant 3
US-11-283-329-221

```

```

Query Match          5.2%; Score 42; DB 8; Length 1417;
Best Local Similarity 69.5%; Pred. No. 1;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```

```

QY 630 CTGAAGGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 689
    |||||
DB 1155 CTTAAAGGAGAGGCTGCTCTTTACTACACCATTTTACTCTTTCTTCTGAATTCATTA 1096
    |||||
QY 690 CTTCTTGTAGATTAAGTTCTGT 711
    |||||
DB 1095 CTTCTTGTATATATCAATTTCTTT 1074
    |||||

```

```

RESULT 34
US-11-266-748A-349577/C
; Sequence 349577, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptional Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03

```

```

; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 349577
; LENGTH: 1943
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-349577
```

```

Query Match      5.2%; Score 42; DB 8; Length 1943;
Best Local Similarity 69.5%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```

Qy      630 CTGAAGGAGAGGCTGCTCTTTACTACACCAATTTTGTCTTCTTCTGAATTCATTA 689
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      936 CTAAAGGAGAGGCTGCTCCCGGTATACCTCATTCTTGTTCTCTCCCAAGTCATTA 877
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      690 CTTCTTGTAGATAGTCTCT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      876 CTTCTTATATATCATATCTTT 855
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 35

```

US-11-266-748A-382413/c
; Sequence 382413, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Paul
; APPLICANT: Harkin, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 382413
; LENGTH: 1943
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-382413
```

```

Query Match      5.2%; Score 42; DB 8; Length 1943;
Best Local Similarity 69.5%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```

Qy      630 CTGAAGGAGAGGCTGCTCTTTACTACACCAATTTTGTCTTCTTCTGAATTCATTA 689
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      936 CTAAAGGAGAGGCTGCTCCCGGTATACCTCATTCTTGTTCTCTCCCAAGTCATTA 877
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      690 CTTCTTGTAGATAGTCTCT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      876 CTTCTTATATATCATATCTTT 855
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 36

```

US-11-266-748A-432956
; Sequence 432956, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 432956
; LENGTH: 1943
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-432956
```

```

Query Match      5.2%; Score 42; DB 8; Length 1943;
Best Local Similarity 69.5%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy      630 CTGAAGGAGAGGCTGCTCTTTACTACACCAATTTTGTCTTCTTCTGAATTCATTA 689
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1008 CTAAAGGAGAGGCTGCTCCCGGTATACCTCATTCTTGTTCTCTCCCAAGTCATTA 1067
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      690 CTTCTTGTAGATAGTCTCT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1068 CTTCTTATATATCATATCTTT 1089
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 37

```

US-11-266-748A-24382/c
; Sequence 24382, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
```

Query Match	5.2%;	Score 41.2;	DB 8;	Length 807;
Best Local Similarity	49.5%;	Pred. No. 1.5;		
Matches 106;	Conservative 0;	Mismatches 108;	Indels 0;	Gaps 0
QY	296	ACATGACCTTGATGTC	CAAAAGGCGCATYATG	CGCTGAAITTTGATGAGCACAATTACC 355
DB	594	AAATTACAGATATTAA	TATATATCCCTCGCGCCCTGCGCATTTTAA	GACATCTTTT 653
QY	356	CTTTAGCCGATGTTAA	CATTTCTTGAGATTCATTA	CTATTAAATATTATGAAAA 415
DB	654	GTTTACCTTATTTAA	GATTTTTTTTAACTCTCTGTTGTATTA	ATTAATTTTGACCTAAAT 713
QY	416	GTTTTGTCCGTGAT	CATTACCATTCAGATTAATC	GAAATGCAATGCGACACTGAATATCAA 475
DB	714	ATCTGGAATTTCT	CTTTTCTCTCTATAGAGATTGAG	AGAAATTAAAAAAAAAAAAAA 773
QY	476	AAGAAATTAAC	TAAATCATTTTA	GAGACACA 509
DB	774	AAAAAAAAAAAA	ATTAATAAAAAAAAAAAAAA	AAAA 807

QY	371	ACATTTCTTCGAGTTCATTACTATTAATAATTAATTATGAAAAAGTTTTGTCTCGAT	430
Db	345	AAATTATCAACAGTCATCTTCATAATTGAAAAAGTGTTCAGAACTTTGGATCTATTT	286
QY	431	CATTACACATCAATATCATGAAATGAAACGACACTGTAATATCAAAAGAAATATAACTAA	490
Db	285	CATGTATTAATTAAGCCTTAAGTTGTGGACCTTTATCTTATATATACATATAAAA	226
QY	491	AATCATATTAAGACACACACATGTGATTTGTCCATCTGCTCTTTAAGCAATGTTATG	550
Db	225	AATTGTATACGCTTAATTAATTTTTCGATTTGTTCCAATGAGGTTTTTTTGTGTTTG	166
QY	551	TTATTTCTTGCAACCCCTACACAAAGGCCAAGAATT	587
Db	165	TTTATTTGTACATCAATAAGATAGTGTAAATATT	129


```
/ Sequence 134, Application US/10539228
/ Publication No. US20060154250A1
/ GENERAL INFORMATION:
/ APPLICANT: David W. Morris
/ APPLICANT: Marc S. Malandro
/ TITLE OF INVENTION: Novel Compositions and Methods in Cancer
/ FILE REFERENCE: CHIR0052-101 (P023370.0003)
/ CURRENT APPLICATION NUMBER: US/10/539,228
/ PRIOR FILING DATE: 2005-06-17
/ PRIOR APPLICATION NUMBER: US 10/322,281
/ PRIOR FILING DATE: 2002-12-18
/ NUMBER OF SEQ ID NOS: 866
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 134
/ LENGTH: 139326
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(139326)
/ OTHER INFORMATION: n = A,T,C or G
US-10-539-228-134
```

```
Query Match
Best Local Similarity 5.1%; Score 40.8; DB 6; Length 139326;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
```

```
QY 296 ACATTGACCTGATGTCGCAAAAGGCGATTGTGCTGCAATTTGATGAGCAGCATTACC 355
DB 58662 ACACCTTACAAATGGCAAAAGCTCGAATAGACATTTCTCCAAAGATATTAATGCGC 58603
QY 356 CTTTGGCCATGTTACATTTCTTGAGATTCATTAATTAATTTATGAAAA 415
DB 58602 AATGACCATTAAGAAAGATATTTACATCATTAATTAATTAATTAATTAATTAAT 58543
QY 416 GTTTTGTCTGATCATTCATCAGATCAAGATTAATCAAGATGACCACTG 467
DB 58542 CATAAGAAAGCTGCTCATACCCATTAGATTAATTAATTAATTAATTAATTAATTAAT 58491
```

```
RESULT 41
US-11-222-810-10
/ Sequence 10, Application US/11222810
/ Publication No. US20060089490A1
/ GENERAL INFORMATION:
/ APPLICANT: MUNNICH, Arnold
/ APPLICANT: Munnich, Judith
/ TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
/ FILE REFERENCE: 2121-0140P
/ CURRENT APPLICATION NUMBER: US/11/222,810
/ PRIOR FILING DATE: 2005-09-12
/ PRIOR APPLICATION NUMBER: US/09/109,082
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 08/545,196
/ PRIOR FILING DATE: 1995-10-19
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 10
/ LENGTH: 1582
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-222-810-10
```

```
Query Match
Best Local Similarity 5.0%; Score 40.4; DB 8; Length 1582;
Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
```

```
QY 364 CATGTTAATCATTTCTTCAGATTCATTAATTAATTAATTAATTAATTAATTAAT 423
DB 1423 CATGTTAATCATTTCTTCAGATTCATTAATTAATTAATTAATTAATTAATTAAT 1482
QY 424 CTTGATCATTTACATCAAGATTAATCAAGATTAATCAAGATTAATCAAGATTAAT 483
```

```
DB 1483 TTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1542
QY 484 AAACATAAATCATTAATAGACACAA 509
DB 1543 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1568
```

```
RESULT 42
US-11-222-810-12
/ Sequence 12, Application US/11222810
/ Publication No. US20060089490A1
/ GENERAL INFORMATION:
/ APPLICANT: MUNNICH, Judith
/ APPLICANT: Munnich, Arnold
/ TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
/ FILE REFERENCE: 2121-0140P
/ CURRENT APPLICATION NUMBER: US/11/222,810
/ PRIOR FILING DATE: 2005-09-12
/ PRIOR APPLICATION NUMBER: US/09/109,082
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 08/545,196
/ PRIOR FILING DATE: 1995-10-19
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 12
/ LENGTH: 1582
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-222-810-12
```

```
Query Match
Best Local Similarity 5.0%; Score 40.4; DB 8; Length 1582;
Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
```

```
QY 364 CATGTTAATCATTTCTTCAGATTCATTAATTAATTAATTAATTAATTAATTAAT 423
DB 1423 CATGTTAATCATTTCTTCAGATTCATTAATTAATTAATTAATTAATTAATTAAT 1482
QY 424 CTTGATCATTTACATCAAGATTAATCAAGATTAATCAAGATTAATCAAGATTAAT 483
DB 1483 TTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1542
QY 484 AAACATAAATCATTAATAGACACAA 509
DB 1543 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1568
```

```
RESULT 43
US-11-266-748A-41216/C
/ Sequence 41216, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ PRIOR FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
```

```

? PRIOR FILING DATE: 2005-03-14
? PRIOR APPLICATION NUMBER: US 60/700,293
? PRIOR FILING DATE: 2005-07-18
? NUMBER OF SEQ ID NOS: 48396
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO: 41216
? LENGTH: 557
? TYPE: DNA
? ORGANISM: Homo Sapiens
US-11-266-748A-41216

```

Query Match	5.0%;	Score 39.6;	DB 8;	Length 557;
Best Local Similarity	61.8%;	Pred. No. 3.2;		
Matches 63;	Conservative 0;	Mismatches 39;	Indels 0;	Gaps 0

Dy 696 TGTAGATAACGTTCTGTAGAACAAGCGTGTATTATTAAGAAACAATTATCTTCATC 755
Db 233 TGCAAGTAAATTAATTATGACTGATCTGTAGCATATACAAATMAAAAATTGTCAGTCATC 174

```

QY      756 CACAGGGAATTCATTACTTAATGCCAATAATTACGTTTG 797
          ||| | | | | | | | | | | | | | | |
Db      173 CACAATTAAGTACAATTATTATGAGAAAAATTTTACTATG 132

```

RESULT 44
US-11-266-748A-95203/c
; Sequence 95203, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-95203

Query Match	5.0%	Score 39.6;	DB 8;	Length 559;
Best Local Similarity	61.8%	Pred. No. 3.2;		
Matches	63;	Conservative	0;	Mismatches 39;
				Indels 0;
				Gaps 0

RESULT 45
US-11-266-748A-148014
; Sequence 148014, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

Query Match	5.0%	Score 39.6;	DB 8;	Length 559;
Best Local Similarity	61.8%	Pred. No. 3.2;		
Matches 63;	Conservative 0;	Mismatches 39;	Indels 0;	Gaps 0

Qy 636 TGTGATTAAGTCTCTGTAGCAACAGCTGTCTTATTATAGAAAACAAATTATCTCTTCATC 755

Db 332 TGCAGGTATTTAATTATGACTGATCTGTGGAATATACAAATTAATAATTTGTCAGTCATC 392

Oy 756 CACAGGAAATTCATTACTTAATGCCAATAATTACGTTTG 797
||| ||| ||| ||| ||| |||
Db 392 CACATTAACTACAATTATTATGGAGAAAAATTTTACTATG 433

RESULT 46
US-11-266-748A-117427/c
Sequence 117427, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
PRIORITY FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9

```

PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 117427
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-117427

```

```

Query Match
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```

```

QY 696 TGTAGTAAGTCTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAATTATCTTCATC 755
DB 672 TGCAGGTAATTATTAATGATGCTGATCTGTAGAAATATACATAAATTTGTCAGTCATC 613
QY 756 CACAGGAAATTCATTACTTAATGCCAAATATATTACGTTTG 797
DB 612 CACAATTAACTACATATTATTATGAGAAAAATTTACTATG 571

```

```

RESULT 47
US-11-266-748A-159591
Sequence 159591, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 159591
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-159591

```

```

Query Match
Best Local Similarity 5.0%; Score 39.6; DB 8; Length 1000;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```

```

QY 696 TGTAGTAAGTCTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAATTATCTTCATC 755
DB 329 TGCAGGTAATTATTAATGATGCTGATCTGTAGAAATATACATAAATTTGTCAGTCATC 388

```

```

QY 756 CACAGGAAATTCATTACTTAATGCCAAATATATTACGTTTG 797
DB 389 CACAATTAACTACATATTATTATGAGAAAAATTTACTATG 430

```

```

RESULT 48
US-11-266-748A-222651/C
Sequence 222651, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 222651
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-222651

```

```

Query Match
Best Local Similarity 5.0%; Score 39.6; DB 8; Length 1000;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```

```

QY 696 TGTAGTAAGTCTCTGTAAGAAACAGCTGTGTTATTATAGAAAAACAATTATCTTCATC 755
DB 672 TGCAGGTAATTATTAATGATGCTGATCTGTAGAAATATACATAAATTTGTCAGTCATC 613
QY 756 CACAGGAAATTCATTACTTAATGCCAAATATATTACGTTTG 797
DB 612 CACAATTAACTACATATTATTATGAGAAAAATTTACTATG 571

```

```

RESULT 49
US-11-266-748A-289193/C
Sequence 289193, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4

```

PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 289193
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-289193

Query Match 5.0%; Score 39.6; DB 8; Length 1000;
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 696 TGTAGATAAGTCTCTGTAAGAAACAGCTGTGTATATAGAAACAAATTTATCCTTCATC 755
DB 672 TGCAGTAATTTAATTAATGACTGATCTGTAGGAATATACATTAATAATTTGTCAGTCATC 613
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTG 797
DB 612 CACAATTAAGTACATTAATTTATGAGAAAAATTTTACTATG 571

RESULT 50
US-11-266-748A-340622
Sequence 340622, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkins, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 340622
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-340622

Query Match 5.0%; Score 39.6; DB 8; Length 1000;
Best Local Similarity 61.8%; Pred. No. 3.9;
Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 696 TGTAGATAAGTCTCTGTAAGAAACAGCTGTGTATATAGAAACAAATTTATCCTTCATC 755
DB 329 TGCAGTAATTTAATTAATGACTGATCTGTAGGAATATACATTAATAATTTGTCAGTCATC 388
QY 756 CACAGGAAATTCATTACTTAATGCCAAATTAATTCGTTTG 797
DB 389 CACAATTAAGTACATTAATTTATGAGAAAAATTTTACTATG 430

Search completed: July 19, 2006, 19:51:43
Job time : 169 secs